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Oropouche Peptide # Peptide # Human bon Human bra Human pep Arabidops Novel hum Novel hum Arabidops Arabidops N. gonorr Human nov Human nov Human nov Human sec N. gonorr Helicobac Acinetoba Streptoco Human ORF Human end Human 5' Human end Mammoglob An endome Rice isol Rice isol Arabidops Herbicida Sequence Human ORF Human ova Human end Human end Breast ca Human PRO Human ORF Wheat asp Arabidops Acinetoba Pathogen Human ORF Human pro Human ORF Non-ocula B. thurin Arabidops Arabidops B. thurin Arabidops ритап т Wheat str E. faeciu Protein e Protein e Staphyloc Human end Protein o Human sec Arabidops Human nov Human nov Arabidops Human end MLHR comp Lactococc Arabidops Drosophi] Human ner . thurin Canine lo Aaw99092 Aaw99092 Abb493021 Aam76938 Abg46060 Abg46060 Abg46060 Abg00521 Abg00521 Abg00521 Abg00521 Abb6448 Abb6448 Abb6448 Abb6448 Abb6448 Abb6448 Abb6448 Abb6448 Abb6448 Abb6482 Abb6448 Abb6482 Abb6482 Abb6482 Abb68334 Abb68334 Abb68334 Abb69813 Aab31682 Aac20555 Abg96356 Abb73169 Abr47522 Abc78795 Abc78795 Abb63376 Abb63376 Aae03588 1 Aag34364 Ada36447 Aaw72393 Abp32702 Ada54452 Abb17370 Abu58228 Adc97504 Aay60038 Aau02024 Aag10474 Aag24527 Abr57093 Aau02025 Abb54747 Abb54747 Abb11397 Aag27381 Abb81063 Aag01456 Aag34531 Aau16559 Abu55628 Aag06674 AAG24529
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KW diabetes; Cushing's disease; eating disorder; AIDS; XX XX OX Synthetic. Location/Qualifiers FH Key FT Misc-difference Location/Qualifiers FT Misc-differe	Controlling the availability and cell surface receptor, useful for Claim 10; Page 27; 36pp; English This sequence is a binding site controlling the availability and surface receptor by administern inhibiting proteolytic cleavage proteolytic cleavage results in surface for longer and therefore the cell. This increases the ser might be present. The binding method is either derived from, omotif. The inhibitor may be used disorders such as renal tubular syndrome, cachexias, eating discusty Match	Similarity 100.0%; 3; Conservative 0 XEFIXXDX 8 Standard, peptide; 12 standard, peptide; 12 bulin E (IgE) receptc ansduction; proteolyt te binding site; muscl Cushing's disease; e reconnection of the context of
	Add36041 Acinetoba Abb50024 Listeria Abm65964 Photorhab Aag41175 Arabidops Aag41208 Arabidops Aag41208 Arabidops Aag411114 Arabidops Aag411114 Arabidops Aag511126 Arabidops Aag51126 Arabidops Aag51126 Arabidops Aag51126 Arabidops Aag51126 Arabidops Aag51126 Arabidops Aay6099 Amino aci Aaw5069 Amino aci Aaw5069 Kitebsiall Aaw60261 Kitebsiall Aaw6170 Cyteolic Aab58174 Lung canc Aab54702 Human sec Aab54302 Human sec Aab7488 Saccharom Abu26653 Protein e Aag10426 Aay34658 Chlamydia	Aag92223 Aag92259 Aag92259 Aag12207 Aag43174 Cleavage.
226 1 AAP900048 226 1 AAP90122 226 1 AAP90122 226 5 ABD489342 226 6 ABU04231 226 6 ABU04231 227 4 AAU34185 229 6 ABW68207 229 6 ABW68207 229 7 AACS1648 231 2 AAV23625 233 3 AACS1648 233 3 AACS1659 233 3 AACS1659 234 4 ABB65699 234 4 ABB65699 234 6 ABP3713 236 6 ABP3713 236 6 ABP36273 237 3 AAB16523 238 2 AANF6226	• N O M M M M M M M M M M M M M M M M M M	4 AAG92223 4 AAG92359 4 AAG922359 3 AAG12207 3 AAG43174 ALIGNMENTS e; 8 AA. n inhibition of eolytic cleavage muscle wasting;
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98EP-00200799.
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          WPI; 1999-510568/43.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Sequence 12 AA;
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                                                                                                                                                                                                                                  This sequence is a polypeptide from the immunoglobulin E receptor.

Sequences (AAY32794-Y32823) are examples of polypeptide sequences found

at or near the ubiquitin/proteosome complex binding site located on the

intracellular part of a cell surface receptor. These sequences are used

in a method for controlling the availability and signal transduction

capability of a cell surface receptor by administering an inhibitor that

capability of a cell surface receptor by administering an inhibitor that

capability of a cell surface receptor by administering an inhibition

confirmed to inhibiting proteclytic cleavage of the receptor. Inhibition

of this proteclytic cleavage results in the receptors being present on

the surface for longer and therefore signalling for longer to the

the surface for longer and therefore signalling for longer to the

confirmed to capability this increases the sensitivity of cells to any

competes with or binds to a polypeptide sequence of which sequences

AAY32794-Y32823 are examples. The inhibitor may be used to treat muscle

wasting, associated with disorders such as renal tubular defects,

curaemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS,

after stress and during neuromuscular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal transduction, proteolytic cleavage, growth hormone receptor, proteosome binding site, muscle wasting, renal tubular defect, uraemia, diabetes, Cushing's disease, eating disorder, AIDS; ubiquitin;
                                                                                                                                                                          Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth hormone receptor derived polypeptide.
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                                                                                                                                                                                                                 Disclosure; Page 9; 36pp; English.
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GEFIWVDG 12
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                                                                            12-MAR-1998;
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                           EP943624-A1
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   Synthetic.
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This sequence is derived from the growth hormone receptor polypeptide
AAY32792. This sequence and variants (AAY32794-Y32823) of it are examples
of polypeptide sequences found at or near the ubiquitinfyroteosome
controlled to the intracellular part of a cell surface
receptor. These sequences are used in a method for controlling the
availability and signal transduction capability of a cell surface
receptor by administering an inhibitor that is capable of inhibiting
proteclytic cleavage of the receptor. Inhibition of this proteclytic
cleavage results in the receptors being present on the surface for longer
and therefore signalling for longer to the interior of the cell. This
increases the sensitivity of cells to any hormones which might be
the inhibitor is either derived from, competes with or binds to
a polypeptide sequence of which sequences AAV3294-Y32823 are examples.
The inhibitor may be used to treat muscle wasting, associated with
disorders such as renal tubular defects, uraemia, diabetes, Cushing's
syndrome, cachexias, eating disorders, AIDS, after stress and during
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Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
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Pred. No. 1.8e+02;
Mismatches 0; Indels
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                                                                                                                                                                   Disclosure; Page 5; 36pp; English.
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; signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, of which this sequence is an example, is located at or around a ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this Signal transduction, proteclytic cleavage, growth hormone receptor; protecosome binding site, muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency; inhibitor. Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies. of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease Gaps .; 0 Score 25, DB 2; Length 12; Pred. No. 1.8e+02; ; Mismatches 0; Indels Chicken growth hormone receptor derived polypeptide. Disclosure; Page 9; 36pp; English. AAY32794 standard; peptide; 12 AA 100.0%; Sc 50.0%; Pre cive 4; 98EP-00200799. 98EP-00200799 (first entry) (UYUT-) RIJKSUNIV UTRECHT Conservative Query Match
Best Local Similarity
4; Conserve : | | | :: |: 5 VEFIELDI 12 ω WPI; 1999-510568/43. 1 XEFIXXDX Sequence 12 AA; Gallus gallus 12-MAR-1998; 12-MAR-1998; 09-NOV-1999 EP943624-A1 22-SEP-1999 AAY32794; RESULT 5 a

This sequence is a polypeptide from the chicken growth hormone receptor.
Sequences (AAY32794-Y32823) are examples of polypeptide sequences found
at or near the ubiquitan/proteosome complex binding site located on the
intracellular part of a cell surface receptor. These sequences are used
in a method for controlling the availability and signal transduction
capability of a cell surface receptor by administering an inhibitor that
is capable of inhibiting proteclytic cleavage of the receptor. Inhibition
of this proteclytic cleavage results in the receptors being present on
the surface for longer and therefore signalling for longer to the
the surface for longer and therefore signalling for longer to the
the surface for longer and therefore signalling for longer to the
control might be present. The inhibitor is either derived from,
competes which might be present. The inhibitor may be used to treat muscle
AAY32794-Y32823 are examples. The inhibitor may be used to treat muscle
wasting, associated with disorders such as renal tubular defects,

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                                                                                                                                                                                                                                                                                                                                                                                                                              Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MTG; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, rarasporter, cycoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing
uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myeloma, colon cancer, gastric cancer, adenocarcinomy, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed
                                                                                                                            Gaps
                                                                                                                            .;
0
                                                                                         Length 12;
                                                                                                                           0; Indels
                                                                                     Score 25; DB 2;
Pred. No. 1.8e+02;
4; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                Human expressed protein tag (EPT) #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 73; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urban RG;
                                                                                                                                                                                                                                                                                  ABU03293 standard; protein; 13 AA.
                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0279495P.
2001US-0292544P.
2001US-0310801P.
2001US-0326370P.
2001US-0336780P.
                                                                                       100.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2002; 2002US-0358985P
                                                                                                                                                                                                                                                                                                                                                         29-JAN-2003 (first entry)
                                                                                                                           Conservative
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                                                                                                                                                                                 :|||::|:
5 VEFIELDI 12
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                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                            1 XEFIXXDX
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                                                    Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200278524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2001;
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08-AUG-2001;
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04-DEC-2001;
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                                                                                                                                                                                                                                                                                                                       ABU03293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukemia
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ABP42844 standard; protein; 36
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specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assays for identifying regulators of cell cycle progression - comprise expressing a protein having a transcription factor nuclear localisation signal and determining the degree of nuclear localisation.
                                                                                                                                                                                                    Gaps
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                                                                                                                                               Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine DP-3 protein E region nuclear localisation signal.
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying; cell cycle regulator; E region; DP-3 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear localisation signal; NLS; mouse; murine.
                                                                                                                                         Score 25; DB 6;
Pred. No. 1.9e+02;
                                                                                                                                                                                                       Mismatches
                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW33004 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 57; 65pp; English.
                                                                                                                                                                                                       4 ;
                                                                                                                                               100.0%;
50.0%; I
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                                                                                                                                                                                                       Conservative
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GEFIWVDG 9
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Best Local Similarity
Matches 4; Conserv
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                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             La Thangue NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9743647-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1997;
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                                                                                                                                            Query Match
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The invention relates to 2175 novel human ovarian antigens (ABB41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynoclocides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynocleotides against human ovarian antigens and the use of ovarian antigen polynocleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clisorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired framenosus), blood-related disorders (e.g., anaemia), cardiovascular disorders of and urinary system disorders. Ovarian antigen polypeptides and disorders ovarianty systemic lumined which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynuclectides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynuclectides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypoptides may be used as food additives or to prepare antibodies useful in disease diagnosis, druq targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                            gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; gynaecological; reproductive.
                                                                                         Human ovarian antigen HPCRN90, SEQ ID NO:3976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 3976; 2922pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2001; 2001WO-US018569.
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABQ55921
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200200677-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                               22-AUG-2002
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(first entry)

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Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes encoding secreted polypeptides.
                                                                Human secreted protein encoded by gene 96.
AAY36319 standard; protein; 45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-418749/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX98011
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18-DEC-1997;
18-DEC-1997;
18-DEC-1997;
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                         W09931117-A1
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19-DEC-1997;
19-DEC-1997;
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                                           17-SEP-1999
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18-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore PA,
                     AAY36319
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kyaw H,
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AXX30724 to AXX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0100993. These genomic DNA sequences encode the novel proteins given in AXY1114 to AAX11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a protective immune response in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding pneumococcal polypeptide(s) - useful in vaccines,
                                                                   Gaps
                                                                                                                                                                                                                                                         pneumoniae strain 0100993; vaccine; immune response; infection; pneumococcal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 2; Length 37; 50.0%; Pred. No. 5.7e+02; ive 4; Mismatches 0; Indels
                                            Length 36;
                                         Score 25; DB 5; Length 36
Pred. No. 5.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                      Streptococcus pneumoniae protein sequence ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholas RO,
 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knowles DJC,
                                                                                                                                                                    AAY11253 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 279; 354pp; English.
                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                           100.0%; E
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96US-0025788P.
                                                                                                                                                                                                                                                                                                                                                               97WO-US005306
                                                                                                                                                                                                                (first entry)
                                                                 Conservative
                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
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                                                                                                    :|||::|:
QEFIDDDK 20
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                                                                                       1 XEFIXXDX 8
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37 AA;
                      Sequence 36 AA;
                                                                                                                                                                                                                                                                        streptococcal
                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1996;
                                                                                                                                                                                                                                                                                                                   W09737026-A1
                                                                                                                                                                                                                                                                                                                                                               01-APR-1997;
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                                                                 4;
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                                                                 Matches
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97US-0068006P. 97US-0068001P. 97US-0068053P. 97US-0068054P. 97US-0068054P. 97US-0068054P. 97US-0068054P. 97US-0068169P. 97US-0068169P.

97US-0068368P 97US-0068369P

98WO-US027059

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AXY97916 to AAX98029 represent 110 isolated human secreted protein genes.
AXY36224 to AAX16727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating secreted polypeptides are useful for preventing the amount of the new polypeptides in a sample or by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most nightly expressed in, and include developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune discases, inflammation, allergies, Altheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovacular disorders, kidney disorders, atherosclerosis, diabetes, cardiovacular disorders, kidney disorders, disouse also useful for identifying their binding partners. The polypeptides are also useful for identifying their binding partners. The sequences given in AAX97907 to AAX97915 and AAX16223 are used in the exemplification of
Claim 11; Page 401; 537pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention
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DB 2; Length 45;

100.0%; Score 25; DB 2, 50.0%; Pred. No. 7e+02;

Query Match Best Local Similarity

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Gaps

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4; Conservative

Matches

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RESULT 10 AAY36319

1 XEFIXXDX 8

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Feng P;

Soppet DR; Greene JM,

, Rosen CA, Florence C,

Shi Y,

Ruben SM, Carter KC, Shi Y, ei Y, Florence K, Duan RD, v., G. Janat F, Ni J;

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Gaps

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Indels

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06-NOV-2003

ADA11680;

RESULT 11 ADA11680 20-MAR-2003

Homo

18-DEC-1997,

18-DEC-1997, 18-DEC-1997, 18-DEC-1997 18-DEC-1997

18-DEC-1997 18-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 17-JUN-1999

Moore PA,

disorders

7e+02;

Matches

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The present sequence is that of amino acids 7-54 of a phospholipid transporter consensus sequence, denoted ATPase hydrolase phosphorylation transporter consensus sequence, denoted ATPase hydrolase phosphorylation. This sequence shows 56% identity with a phospholipid-transporting multigene. This sequence shows 56% identity with a phospholipid-transporter of the invention, designated 6710% (see ABP72495). The invention provides 6710% nucleic acids and polypeptides, vectors, host cells, antibodies and transgenic animals. The 6170% nucleic acids and polypeptides are useful for diagnosing, preventing or treating conditions related to aberrant activity or deficient phospholipid transporter function or expression, such as neurological disorders, callular proliferative and/or differentiative disorders, immume disorders, inflammatory disorders, viral diseases, cardiovascular disorders, blood coagulation disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New 61708 nucleic acid molecules and polypeptides, useful for diagnosing or treating conditions related to aberrant activity or deficient phospholipid transporter function or expression, e.g. autoimmune disease,
    increase or decrease storage capabilities, fat content or other untritional components. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
                                                                                                                                                                                                             Score 25; DB 6; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phospholipid transporter; ATPase; enzyme; 67108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phospholipid transporter consensus sequence.
  decrease storage capabilities,
                                                                                                                                                                                                                                Pred. No. 7e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 66; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP72498 standard; protein; 48 AA.
                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                  50.0%;
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                                                                                                                                                                                                                                                         4; Conservative
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Best Local Similarity
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                                                                                                                                                                   AA;
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                                                                                                                                                                   Sequence 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP72498;
                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated HXABT24 nucleic acid molecule. The polypeptides, mucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for thromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunological probes for differential identification of the tissues immunological probes for differential identification decreases and antiagonist may also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New secreted HKABT24 nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soppet DR;
Greene JM,
       ·.
                                                                                                                                                                                                                                                                                                                                                                                cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; food preservative; storage capability; fat content; nutritional component; human; secreted protein.
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carter KC, Shi Y, Rosen CA,
ence KA, Duan DR, Florence C,
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                                                                                                                                                                                                                                                                                                                                         Human novel secreted protein, SEQ ID NO 208.
Mismatches
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                                                                                                                                                                                                    ADA11680 standard; protein; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Florence KA, Duar
Janat F, Ni J;
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97US-0068008P.
97US-0068053P.
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97US-0068064P.
97US-0070923P.
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97US-0068365P.
97US-0068367P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00334595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US027059
                                                                                                                                                                                                                                                                                          (first entry)
  4; Conservative
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                                            1 XEFIXXDX
                                                                                      25 IEFIAADF
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Ferrie AM, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADA11556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
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Gaps

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Length 48;

100.0%; Score 25; DB 6; Length 48 50.0%; Pred. No. 7.5e+02; ive 4; Mismatches 0; Indels

4; Conservative

Matches

Peptide #3126 encoded by probe for measuring cervical gene expression. human; microarray; gene expression; cervical epithelial cell;

cervical cancer.

Probe;

WO200157278-A2.

09-AUG-2001

Homo sapiens.

(first entry)

12-OCT-2001

AAM16692;

AAM16692 standard; protein; 56 AA.

RESULT 14 AAM16692

:|||::|: GEFIWVDG 18

11

g

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Protein comprising a variant of model C-type lectin-like domains (CTLD), in which alpha helices, beta-strands, connecting segments are conserved to maintain CTLD scaffold structure, while the loop region is altered.
                                                                                                                                        Scaffold protein; C-type lectin-like domain; CTLD; alpha-helix; beta-strand; connecting segment; 14loop region; tetranectin; ligand-binding specificity; human; mouse; rat; chicken; trout; cow.
                                                                                                                                                                                                                                                                                                         Thogersen HC;
                                                                                                                       C-type lectin-like domain protein IGE-FCR.
                                                                                                                                                                                                                                                                                                        Holtet TL, Graversen NJH,
                                                              ABG80735 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 5; 168pp; English.
                                                                                                                                                                                                                                                       13-DEC-2000; 2000DK-00001872.
28-FEB-2001; 2001US-0272098P.
                                                                                                                                                                                                                                     13-DEC-2001; 2001WO-DK000825.
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                    (BORE-) BOREAN PHARMA AS
           : | | | :: | :
DEFIPADL 26
1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                          WPI; 2002-643278/69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derivatives may
CTLD protein of
                                                                                                                                                                                                WO200248189-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54 AA;
                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                       Etzerodt M,
                                                                                                    29-NOV-2002
                                                                                                                                                                                                                   20-JUN-2002.
                 19
                                                                                  ABG80735;
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Rank DR;

Chen W,

Hanzel DK,

Penn SG,

NPI; 2001-488901/53

(MOLE-) MOLECULAR DYNAMICS INC

2000GB-00024263

04-OCT-2000;

03-AUG-2000; 2000UG-00632366. 21-SEP-2000; 2000UG-0234687P. 27-SEP-2000; 2000US-0236359P.

30-JAN-2001; 2001WO-US000670.

2000US-0180312P. 2000US-0207456P. 2000US-00608408.

04-FEB-2000; 26-MAY-2000; 30-JUN-2000;

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ABB35677 standard; peptide; 56 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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The present invention relates to a new protein with scaffold structure of c-type lectin-like domains (CTLD). The invention comprises a variant of a model CTLD where alpha-helices and beta-strands and connecting segments are conserved such that scaffold structure of C-type lectin-like domains are conserved such that scaffold structure of C-type lectin-like domains (CTLD) is substantially maintained, while the 14loop region is altered by amino acid substitution, deletion, insertion or their combination. The invention is useful for preparing a library of nucleotide sequences convention is useful for preparing a library of nucleotide sequences invention is proteins by randomising part or all of the nucleic acid proteins by randomising part or all of the nucleic acid proteins products are preferable to antibody derivatives as each binding components of compositions to be used for in vivo diagnostic or therapeutic purposes, arrificial CTLD protein products constructed on the basis of human CTLDs are virtually identical to the corresponding natural communogenic to the patient. They also have a smaller size, and thus immunogenic to the patient. They also have a smaller size, and thus crowing specificatly defining of polypeptide segments defining clayatives may be achieved. The present amino acid sequence represents a curring of privatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 5; Length 54; 50.0%; Pred. No. 8.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SERPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 4; Length 56;
Pred. No. 8.8e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.8e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 21518; 487pp; English.
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HXXXH
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0

Gaps

0;

Matches

30-JUN-2000;

Penn SG,

Human gene

04-FEB-2000; 26-MAY-2000;

Homo sapiens

09-AUG-2001

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful
                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #3165 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 56;
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4; Mismatches
                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 29448; 654pp; English.
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                                                                                                                                                               Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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             26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SBP-2000; 2000US-0234687P.
27-SBP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
2000US-0608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                               Chen W,
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2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            human genetic disorders
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QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-496933/54
                                                                                                                                                                Hanzel DK,
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                               WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                Penn SG,
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ABB30514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and sipplaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #3216 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                 Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                    Peptide #3183 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 28312; 639pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in human fetal liver
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50.0%; E
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                    2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157272-A2
                                                                                                                         WO200157277-A2.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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17-0CT-2001

AAM29179;

RESULT 16 AAM29179

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09-AUG-2001.

0

Gaps

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide economic but was obtained in electronic format directly from WIPO
for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                SEQ ID NO 13482; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56 AA;
                                                                                Claim 27;
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Score 25; DB 4; Length 56; Pred. No. 9.8e+02; Mismatches 0; Indels Pred. No. 8.8e 4; Mismatches 100.08; 50.0%; 4; Conservative :|||::|: QEFINLDG 44 1 XEFIXXDX 8 Local Similarity Query Match Matches à 엄

ABB21106 standard; protein; 56 AA. ABB21106; RESULT 18 ABB21106

(first entry) 23-JAN-2002

Protein #3105 encoded by probe for measuring heart cell gene expression.

Human, gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.

Homo sapiens

WO200157274-A2

09-AUG-2001

30-JAN-2001; 2001WO-US000666 2000US-0180312P 04-FEB-2000;

26-MAY-2000; 2000US-0207456F. 30-UUN-2000; 2000US-00608408 03-AUG-2000; 2000US-00632866. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-02368359P. 2000US-0236359P. 2000GB-00024263. (MOLE-) MOLECULAR DYNAMICS INC.

04-OCT-2000;

Rank Chen W, Hanzel DK, WPI; 2001-488899/53 Penn SG,

DR;

Single exon nucleic acid probes for analyzing gene expression in human hearts.

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e-g. cardiovascular diseases of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                 Claim 15; SEQ ID NO 22876; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AA;
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Gaps . 100.0%; Score 25; DB 4; Length 56; 50.0%; Pred. No. 8.8e+02; ive 4; Mismatches 0; Indels Conservative 37 OFFINEDG 44 æ Local Similarity
les 4; Conserv 1 XEFIXXDX Query Match Matches ð g

0;

RESULT 19 AAM68870

. 0

Gaps

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AAM68870 standard; protein; 56 AA. AAM68870; Human bone marrow expressed probe encoded protein SEQ ID NO: 29176. pone Human;

(first entry)

06-NOV-2001

marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma. WO200157276-A2. microarray; Homo

09-AUG-2001

2000US-0207456P. 2000US-00608408. 2000US-00632366. 30-JAN-2001; 2001WO-US000668. 2000US-0234687P 2000US-0236359P 2000GB-00024263 04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

(MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

Example 4; SEQ ID NO 29176; 658pp + Sequence Listing; English.

probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention The present invention provides a number of single exon nucleic acid

Sequence 56

XX 08

4,

Matches

AAM56491;

AAM56491 RESULT

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG4734e-ABG59930 represent human liver single exon encoded peptides of the invention. Note The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fig., wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #3091 encoded by probe for measuring breast gene expression.
                                                                                                                                Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 4; Len
A No. 8.8e+02;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 29179; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                Human liver peptide, SEQ ID No 29179
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ABGS0531 standard; peptide; 56 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                       , 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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                                                                   (first entry)
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37 QEFINLDG 44
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                         Homo sapiens.
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                                     ABG50531;
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Matches
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                                                                                         0
                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 28596.
                                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer
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                                                          Length 56;
                                                                                           Indels
                                                         Score 25; DB 4; L
Pred. No. 8.8e+02;
4; Mismatches 0;
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                                                                                                                                                                                                                                                   AAM56491 standard; protein; 56 AA.
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26-MAX-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633667P.
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                                                          100.08;
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37 QEFINLDG 44
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Best Local Similarity
                                                              Query Match
Best Local Similarity
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21-SEP-2000; 2
27-SEP-2000; 3
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Penn SG, (MOLE-)

RESULT 21 ABG50531

Matches

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Gaps

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Length 56; Indels primary ciliary dyskinesis; pulmonary hypertension;

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognesing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include breast cancer, disorders of development inflammatory diseases include breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for obtained in electronic form part of the printed specification, but was chemical in the contraction of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel single exon nucleic acid probe used to measuring gene expression in
                                  inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                  Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 13149; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
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26-MX-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00609408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                           29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
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                                                                                                      WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a human breast
                                                                       Homo sapiens
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0
; Score 25; DB 4; Length 56; Pred. No. 8.8e+02; 4; Mismatches 0; Indels
100.08;
           50.08;
                        4; Conservative
           Best Local Similarity
Query Match
                      Matches
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Human peptide encoded by genome-derived single exon probe SEQ ID 28116. chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; Human; single exon probe, asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; ABG38451 standard; peptide; 56 AA. (first entry) :|||::|| 37 QEFINLDG 44 1 XEFIXXDX 8 19-AUG-2002 ABG38451; RESULT 23
ABG38451
ID ABG38
XX
AC ABG38
DT 19-AU
XX
XX
KW HUMAR
KW CAPPORT

Length 56;

100.0%; Score 25; DB 5; 50.0%; Pred. No. 8.8e+02;

100.08;

Query Match Best Local Similarity

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The invention features to a spatially-addressable set or single exon mucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic phound to each probe of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote; burg mentioned microarray; assigning exons to a single exon probe thaving a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single comprising one collective microarrays mentioned in the specification, or encoded by the corpobes/open reading frames (ORP). The probes are used for identifying exons in a gene, particularly using human cancer, chronic obstructive pulmonary diseases (DOPD), interstrial lung dienses, duseases (ILD), familial idiopathic pulmonary fibrosis, encoreded by the rule rule mulmonary and encoded by the rule mulmonary and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histicocytosis, lymphangiolelomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 28116; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR
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30-UTN-2000; 2000US-02608408.
03-AUG-2000; 2000US-00532466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345897P.
04-OCT-2000; 2000GB-00024263.
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                         hyaline membrane disease.
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                                                                         Homo sapiens.
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                                                                                                                                                                    15-NOV-2001
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Matches

à 음 RESULT 24

AAG02282

Human;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                  Arabidopsis thaliana protein fragment SEQ ID NO: 8815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9905-0134768P.
9905-0134941P.
9905-0135323P.
9905-0135629P.
9905-0136629P.
9905-0136782P.
9905-0136782P.
9905-0137528P.
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9905-0137528P.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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99US-0127462P.
99US-0128234P.
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99US-0129845P.
99US-0130077P.
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99US-0131449P.
                                                                                                                                                                                                                                                                                                                                                                             99US-0130449P
                                                                                                                                                                                                     2000EP-00301439
           17-OCT-2000 (first entry)
                                                                                                                    Arabidopsis thaliana
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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                                                                                                                                                EP1033405-A2
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                                                                                                                                                                           06-SEP-2000
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07-JUN-19
08-JUN-19
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can threefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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                                                                                                                                                                                                                                 expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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  Indels
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A, Giordano J;
  Mismatches
                                                                                                                                                                                                       Human secreted protein, SEQ ID NO: 6363.
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                                                                                                                        AAG02282 standard; protein; 57 AA
                                                                                                                                                                                                                                                  gene therapy; chromosome mapping.
    4.
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4; Conservative
                                                                                                                                                                               (first entry)
 4; Conservative
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37 QEFINLDG 44
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                            1 XEFIXXDX 8
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                                                                                                                                                                                                                                    5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                      AAG02282;
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99US-0139462P

18-JUN-1999;

AAG10476,

RESULT 25

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AAG10476

Matches

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990S-0139750P.
990S-0139763P.
990S-013963P.
990S-0140353P.
990S-0140353P.
990S-0140323P.
990S-01412842P.
990S-01412842P.
990S-0142037P.
990S-0142037P.
990S-0142037P.
990S-0142037P.
990S-0142037P.
990S-0142037P.
990S-0142038P.
990S-0144333P.
990S-0144333P.
990S-014532P.
990S-014532P.
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990S-014532P.
990S-014533P.
990S-014433P.
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25-AUG-1999;
26-AUG-1999;
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13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
20-AUG-1999;
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20-AUG-1999;
21-AUG-1999;
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21 - 70L - 1999;
22 - 70L - 1999;
22 - 70L - 1999;
22 - 70L - 1999;
23 - 70L - 1999;
23 - 70L - 1999;
18-JUN-1999;
18-JUN-1999;
22-JUN-1999;
23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
29-JUN-1999;
30-JUN-1999;
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01-JUL-1999;
02-JUL-1999;
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12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
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20-JUL-1999;
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27-JUL-1999;
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04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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12-AUG-1999;
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06-JUL-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Pred. No. 8.9e+02;
1; Mismatches 0;
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9905-0151065P.
9905-0151080P.
9905-0151030P.
9905-0151331P.
9905-0151331P.
9905-01513319P.
9905-01513319P.
9905-01513319P.
9905-01513319P.
9905-0154039P.
9905-01553139P.
9905-01553139P.
9905-01553139P.
9905-01553139P.
9905-015659E.
9905-015659E.
9905-0159231P.
9905-0159231P.
9905-01593131P.
9905-01593131P.
9905-015931P.
9905-0160314P.
9905-0160318P.
9905-0160318P.
9905-0160318P.
9905-0160318P.
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ilarity 50.0%; [
Conservative 4,
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IEFICLDL 38
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es 4; Conserv
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29-SEP-1999;
29-SEP-1999;
04-OCT-1999;
06-OCT-1999;
07-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
110-SEP-1999;
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14-0CT-1999
14-0CT-1999
18-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
22-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
26-0CT-1999
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-SEP-1999;
-SEP-1999;
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29-OCT-1999;
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Matches
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Gaps

99US-0140823P. 99US-0140991P. 99US-0141287P. 99US-0141842P. 99US-0142154P.	99US-0142055P. 99US-0142390P. 99US-0142803P	99US-0142920P.	99US-0143542P.	99US-0144005P.	99US-0144085P. 99US-0144086P.	99US-0144325P.	99US-0144331F.	99US-0144333P.	99US-0144335P.	99US-0144352P. 99US-0144632P	99US-0144884P.	99US-0144814P. 99US-0145086P.	99US-0145088P.	99US-U145085F. 99US-0145087F.	99US-0145089P.	99US-014519ZF. 99US-0145145F.	99US-0145218P.	99US-0145224P.	99US-0145913P.	99US-0145918P. 99HS-0145919P	99US-0145951P.	99US-0146386P. 99US-0146388P.	99US-0146389P.	99US-0147038P. 99US-0147204P.	99US-0147302P.	99US-0147260P.	99US-0147303P. 99US-0147416P.	99US-0147493P.	99US-0148171P.	99US-0148319P.	99US-0148565P.	99US-0148684P. 99US-0149368P.	99US-0149175P.	99US-0149426P. 99US-0149722P.	99US-0149723P.	99US-0149902P.	99US-0149930P.	99US-0150884P.	99US-0151065P.	99US-0151066F. 99US-0151080F.	99US-0151303P.	99US-0151438P. 99US-0151930P.
28-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 01-JUL-1999;	02-JUL-1999; 06-JUL-1999; 08-JUL-1999;	09-JUL-1999;	13-JUL-1999; 14-JUL-1999;	15-JUL-1999;	16-JUL-1999; 16-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	20-JUL-1999; 20-JUL-1999;	20-JUL-1999;	21-JUL-1999; 21-JUL-1999;	21-JUL-1999;	22-JUL-1999;	22-JUL-1999;	23-JUL-1999;	23-JUL-1999;	23-JUL-1999; 26-JUL-1999;	27-JUL-1999;	27-JUL-1999; 27-JUL-1999;	28-JUL-1999;	02-AUG-1999; 02-AUG-1999;	02-AUG-1999;	04-AUG-1999;	04-AUG-1999;	05-AUG-1999;	06-AUG-1999; 06-AUG-1999;	09-AUG-1999;	10-AUG-1999;	11-AUG-1999; 12-AUG-1999;	13-AUG-1999;	13-AUG-1999; 16-AUG-1999;	17-AUG-1999;	18-AUG-1999; 20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	26-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	30-AUG-1999;	31-AUG-1999; 01-SEP-1999; 07-SEP 1999;
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sequence. thaliana. ?.		2000EP-0030143	99US-01218251 99US-01231801	99US-0123548E	99US-0126264E	99US-0126785E	99US-0128234E	99US-0128714E	99US-0130077E	99US-0130510E	99US-0130891E	99US-0132048E	99US-0132407E	99US-0132485E	99US-0132486E	99US-0132863E	99US-0134256F	99US-0134219F	99US-0134221F	99US-01343/UE	99US-0134941E	99US-0135353F	99US-0135629F	99US-0136392F	99US-0136782F 99US-0137222F	99US-0137528F	99US-0137724F	99US-0138094F 99US-0138540F	99US-0138847F	99US-0139452P	99US-0139453P	99US-0139454P	99US-0139455P 99US-0139456P	99US-0139457P	99US-0139458P 99US-0139459P	99US-0139460P	99US-U139461P 99US-0139462P	99US-0139463P	99US-0139750P	99US-0139817P	99US-0139899P	99US-0140354P.
termination so Arabidopsis tl EP1033405-A2.	6-SEP-2000.	:00	25-FEB-1999; 05-MAR-1999;	09-MAR-1999;	25-MAR-1999;	29-MAK-1999; 01-APR-1999;	06-APR-1999;	UB-APR-1999; 16-APR-1999;	99	9	66	י פי	0 0 0	9	თ თ	9	99	9	99	9	99	י סי	99	66	28-MAY-1999; 01-JUN-1999;	99	96	9 y 9 y	99	99	99	0	18-JUN-1999; 18-JUN-1999;	00	99	9 6	ע ע ע ע	66	666	9	თ თ	23-JUN-1999; 24-JUN-1999;
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The present invention describes an Oropouche NP (nucleocapsid) protein. The Oropouche virus belongs to the genus Bunyavirus of family Bunyaviride. The Oropouche NP protein can be used to detect anti-NP antibodies, for diagnosis of Oropouche virus infection and for protein is used to design: (i) oligonucleotide primers for diagnostic reverse transcription polymerase chain reaction (RT PCR) of viral RNA infected cell cultures or serum samples; or (ii) probes for hybridisation reactions with viral RNA. Also, the nucleic acid sequence may be used in vaccines to protect against Oropouche virus infection. The present samples coppute virus infection. The present plasmid, which is used in an example from the present invention. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                               New DNA encoding the nucleocapsid protein of Oropouche virus - used for diagnosing Oropouche virus infection and in vaccines against this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 2; Length 58; Pred. No. 9.1e+02; 4; Mismatches 0; Indels
                                                                                                            Wang H;
                                                                                                            Shope RE,
                                                                                                            Tesh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB43221 standard; peptide; 60 AA.
                                                                                                                                                                                                                                         Example 7; Fig 7; 60pp; English.
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50.0%; F
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21-SEP-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
                          98WO-US014887.
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                                                       97US-0052848P.
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                                                                                 (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                            Barrett ADT, Saeed MF,
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41 SEFIFNDV 48
                                                                                                                                       WPI; 1999-132152/11.
N-PSDB; AAX19099.
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Best Local Similarity
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                          17-JUL-1998;
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28-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 3; Length 57; 50.0%; Pred. No. 8.9e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oropouche NP protein fragment from a recombinant plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW99092 standard; protein; 58 AA
                                                                                                                                                                                                                                                                                                                                           99US-0159584P.
99US-0160741P.
99US-0160768P.
99US-0160768P.
99US-0160814P.
              99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-015659P.
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99US-0159330P.
99US-0159331P.
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99US-0161992P.
99US-0161993P.
99US-0162142P.
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                                                                                                                                                                                                                                99US-0159293P
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04-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||::|:
31 IEFICLDL 38
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Best Local Similarity
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Unidentified.
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                                                                                                                                                                                                                                                                     14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
                                                                                                                                                                     06-0CT-1999;
07-0CT-1999;
08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
              13-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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13-0CT-1999
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21-OCT-1999
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25-OCT-1999
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25-OCT-1999
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05-OCT-1999
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26-OCT-1999
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AAW99092
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Gaps

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Indels

Length 60;

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, lenkaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing
     predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 37259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 37259; 658pp + Sequence Listing; English.
                                                                                        ; Score 25; DB 4; L. Pred. No. 9.4e+02; 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 4;
50.0%; Pred. No. 9.4e+02;
:ive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                                                                                                                                                                                 AAM76953 standard; protein; 60 AA.
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                                                                                         100.0%;
50.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000GB-00024263
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                     4; Conservative
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                                                                                                                                                               : | | | :: | :
37 TEFINMDG 44
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37 TEFINMDG 44
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                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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nes 4; Conserv
                                                                                                                                                1 XEFIXXDX
                                                             Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                            AAM76953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                      RESULT 30
                                                                                                                                                                                                                                     AAM76953
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                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #11098 encoded by probe for measuring placental gene expression.
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                                                                                                              Claim 27; SEQ ID NO 35856; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 4; Length 60; 50.0%; Pred. No. 9.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 37330; 654pp; English.
                 DR;
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                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM37061 standard; protein; 60 AA.
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                Chen W,
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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TEFINMDG 44
                DΚ,
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                                         WPI; 2001-483447/52
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Best Local Similarity
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                Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disorder
                                                                                                                                                                                                                                                                      Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe;
                Penn
                                                                                                                                                                                                                                                                                                                               Matches
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DR.

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Gaps

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0; Indels

Length 60;

us-09-660-302e-1.rag

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Human brain expressed single exon probe encoded protein SEQ ID NO: 36233.
                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 36233; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                Rank DR;
                    AAM64128 standard; protein; 60 AA
                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                           26-MAY-2000, 2000US-0207456F.
30-JUN-2000, 2000US-0060B408
03-AUG-2000, 2000US-0053356.
21-SEP-2000, 2000US-0234667P.
27-SEP-2000, 2000US-0236359P.
                                                                                                                                                                                                                                                                                                   2000GB-00024263
                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483446/52
                                                                                                                                                                  WO200157275-A2
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                               05-NOV-2001
                                                                                                                                                                                        09-AUG-2001
                                          AAM64128;
                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                     brains
RESULT 31
           AAM64128
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                              Sequence 60 AA;
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37 TEFINMDG 44
1 XEFIXXDX 8
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SEQ ID No 37263.
           ABG58615 standard; peptide; 60 AA
                                (first entry)
                                          Human liver peptide,
                                25-FEB-2003
                     ABG58615;
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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.

Homo sapiens

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from MIPO at Human genome-derived single exon nucleic acid probes useful for analyzing Claim 27; SEQ ID NO 37263; 658pp; English Chen W, Rank DR; gene expression in human adult liver. (MOLE-) MOLECULAR DYNAMICS INC 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0236359P. 2001WO-US000664 2000GB-00024263 Hanzel DK, WPI; 2001-488898/53 Sequence 60 AA; WO200157273-A2 30-JAN-2001; 04-FEB-2000; 26-MAY-2000; 04-OCT-2000; 09-AUG-2001 Penn SG,

Gaps ; Length 60 Score 25; DB 4; Length 60 Pred. No. 9.4e+02; 4; Mismatches 0; Indels 100.0%; 50.0%; 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

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37 TEFINMDG 44 00 1 XEFIXXDX 임 ₽

ABG46060 standard; peptide; 60 AA.

ABG46060

Human peptide encoded by genome-derived single exon probe SEQ ID 35725 Human; single exon probe; asthma; lung cancer; COPD; ILD; (first entry) 19-AUG-2002 ABG46060;

chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease

sapiens Ношо AAG34535 standard; protein; 61 AA.

AAG34535

AAG34535;

Chen W, Rank DR;

37 TEFINMDG 44

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Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                               measure gene expression in human lung samples.
                                                                                                                                          Claim 27; SEQ ID NO 35725; 634pp; English.
                                             26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                             30-JAN-2001; 2001WO-US000665
                                                                                                 Hanzel DK,
                                                                                                              WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60 AA;
      WO200186003-A2.
                 15-NOV-2001
                                                                                                  Penn SG,
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12397 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12397 open reading frames derived from the 12614 nucleic acid derived from the 12614 nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a euwaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon from comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon tissues and/or cell types using hybridisation to a single exon comprising one of the exons in the tissues and/or cell types using hybridisation or encoded by the corpusion of the exons in the tissues and/or cell types using hybridisation or encoded by the corpusion of the exons in the tissues and/or cell types using hybridisation or encoded by the corpusion of the exons in the tissues and/or cell types using hybridisation or encoded by the corpusion and for identifying exons in a gene; a peptide comprising one of probes/open reading frames (RPP). The prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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100.0%; Score 25; DB 5; Length 60; 50.0%; Pred. No. 9.4e+02; tive 4; Mismatches 0; Indels Sest Local Similarity Query Match

4; Conservative

Matches

1 XEFIXXDX 8

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Gaps

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                            Arabidopsis thaliana protein fragment SEQ ID NO: 42037.
                                                                                                                                                                990S-0126785P
990S-0126785P
990S-0128748P
990S-0128748P
990S-0128748P
990S-0130449P
990S-0130449P
990S-0130449P
990S-0130449P
990S-0130449P
990S-0132484P
990S-0132484P
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99US-0132486P.
99US-0132863P.
99US-0134256P.
99US-0134218P.
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9905 0135124P
9905 013533P
9905 0135629P
9905 0136322P
9905 0137522P
9905 0137528P
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99US-0134370P.
99US-0134768P.
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99US-0138540P.
99US-0138847P.
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99US-0139452P.
99US-0139453P.
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99US-0123548P.
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                                                                                                                    2000EP-00301439
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              (first entry)
                                                                        Arabidopsis thaliana
                                                                                        EP1033405-A2.
                                                                                                                     25-FEB-2000;
               18-OCT-2000
                                                                                                                                                                                                               19-APR-1999;
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04-MAY-1999;
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100.0%; Score 25; DB 3; Length 61; llarity 50.0%; Pred. No. 9.6e+02; Conservative 4; Mismatches 0; Indels 51 1 XEFIXXDX 8 Similarity 4; Conserva : | | | :: | : 44 LEFIEEDE Query Match Best Local S: Matches 4 q ò

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RESULT 35 ABG00521 ID ABG00521 standard, protein, 64 AA. XX

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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17-OCT-2000 (first entry)
                                                                                                       termination sequence
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   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recarion (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format diarectly from WIPO at the sequences of the invention. Once: The sequence data for this electronic format directly from WIPO at the will be added to the printed specification, but was obtained in electronic format diarectly from WIPO at
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                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                    Novel human diagnostic protein #512.
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23-AUG-2000; 2000US-00649167.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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11-MAY-1999

11-APR-1999

11-AP
                                                                                                     25-FEB-2000;
                                         EP1033405-A2
                                                                        06-SEP-2000
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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                               The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                           New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
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                                                                                    Masignani V, Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel secreted protein, Seg ID 1553.
                                                                                                                                                                                                                                                         Disclosure; Page 666; 815pp; English.
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50.0%; P
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2000US-0198123P.
2000US-0205515P.
  12-FEB-2001; 2001GB-00003424
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2000US-0186350P.
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2000US-0214886P.
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                                          (CHIR-) CHIRON SPA
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16 HEFIYPDS
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18-APR-2000; 2
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30-JUN-2000; 2
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02-MAR-2000;
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                                                                                    Fontana MR,
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Pred. No. 1e+03;
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           99US-0154018P.
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990S-0158029P
990S-015923P
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990S-0159295P
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990S-0159331P
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2000US - 0232400F
2000US - 0232401F
2000US - 0233064F
2000US - 0233065F
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2000US - 0234927F
2000US - 0234997F
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2000US-0246619P
2000US-0246611P
2000US-0246611P
2000US-0249613P
2000US-0249207P
2000US-0249209P
2000US-0249210P
2000US-0249210P
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2000US-0249218P
2000US-0249218P
             2000US-0241809P
2000US-0241826P
2000US-0246474P
2000US-0246474F
2000US-0246476P
2000US-0246476P
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2000US-0246478P
2000US-0246478P
2000US-0246524P
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2000US-0246526P
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2000US-0250391P.
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2000US-0251988P.
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2000US-0251479P
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2000US-0251869P
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2000US-0251990P
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17-NOV-2000; 2
17-NOV-2000; 2
01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
20-0CT-2000; 20-0C
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SM Ruben (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-488783/53. N-PSDB; AAS26587.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1553; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(ELISA). Disorders which are diagnosed or treated include autoimmune

(Giseases e.g. theumacoid arthritis, hyperproliferative disorders e.g.

c neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac

arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,

car areas disorders e.g. Alzheimer's disease, infections caused by

bacteria, viruses and fungi and ocular disorders e.g. corneal infection,

can also be used to aid wound healing and epithelial cell proliferation,

can also be used to aid wound healing and epithelial cell proliferation,

cto prevent skin aging due to surburn, to maintain organs before

cransplantation, for supporting cell culture of primary tissues, to

cransplantation, for supporting cell culture of primary tissues, to

cransplantation or preservative to increase or decrease storage

crapabilities, fat content, lipid, protein, carbohydrater vitamins,

cminerals, cofactors and other nutritional components. The present

sequence represents a novel secreted protein of the printed

sequence data for this patent did not form part of the printed
          5555555555555555555555
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Gaps
                         0
 DB 4; Length 68;
           Pred. No. 1.1e+03;
4; Mismatches 0; Indels
 Score 25;
 100.0%;
         50.0%;
                      4; Conservative
         Best Local Similarity
Query Match
                   Matches
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:|||::|: 11 EEFIGGDR 18 1 XEFIXXDX 8 ð

ABP64248 standard; protein; 68 AA. ABP64248; RESULT 40 ABP64248

(first entry) 04-NOV-2002

Human ORF618

Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatcry; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.

Homo sapiens.

US2002082206-A1.

27-JUN-2002.

30-MAY-2001; 2001US-00867550

30-MAY-2000; 2000US-0208427P

(LEAC/) LEACH M D. (MEHR/) MEHRABAN F. (CONL/) CONLEY P B. (TOPP/) TOPPER J N.

LAW D. (LAWD/)

Topper JN, Conley PB, Œ, Leach MD, Mehraban

ä Law

> 2002-626554/67. WPI; 2002-626554/ N-PSDB; ABQ98811.

New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.

Claim 10; SEQ ID NO 1236; 78pp; English.

The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences

2000US-0229345P

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                                                                                         blood
                                                                                                     data
were discovered in human atherogenic cells, in particular in platelets and human unbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, bloo coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was segdata.uspto.gov/sequence.html?bocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neural disorder; immune system disorder; renal disorder; muscular disorder; disorder; disorder; publicat disorder; publications disorder; publication disorder; publication disorder; publication disorder; inflammatory disease; allergic reaction; hyperproliferative disorder; inflammatory disease; allergic reaction; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiallergic; thrombolytic;
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                     ; Score 25; DB 5; Length 68; Pred. No. 1.1e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          ABU55669 standard; protein; 68 AA.
                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human novel polypeptide #756.
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2000US-0220963P.
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2000US-0225758P.
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Best Local Similarity
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CEFIKGDK
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                                                                                                                                                                         Sequence 68 AA;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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01-SEP-2000;
01-SEP-2000;
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14-AUG-2000;
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14-AUG-2000;
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5' EST; expressed sequence tag; secreted protein; cDNA isolation;

Human secreted protein, SEQ ID NO: 5197.

(first entry)

06-OCT-2000

AAG01116;

gene therapy; chromosome mapping

Homo sapiens EP1033401-A2

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The invention relates to human novel polypeptides and their associated therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. inhibiting or preventing neural disorders, inmune system disorders (e.g. system; lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. campaultis, nasal polyps and sinualis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, c.g. congenital heart defects, Ebstein's anomaly and hypoplastic left (e.g. congenital heart disorders (e.g. acute kidney failure and end stage creat disorders (e.g. spendicitis), inflammatory diseases (e.g. septic shock, bursitis and capendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial cifarction) and cancerous diseases. Sequences ABU55748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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                                                                         2000US-0234223P
2000US-0234274P
2000US-0234937P
2000US-0236337P
2000US-0236367P
2000US-0236367P
2000US-0236369P
2000US-0236369P
2000US-0236369P
2000US-0236369P
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2000US-0240960P.
2000US-0241785P.
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2000US-0237039P.
2000US-0237040P.
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2000US-0244617P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABX73928
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
03-0CT-2000;
03-0C
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29-SEP-2000;
29-SEP-2000;
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27-SEP-2000;
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Giordano J;

Duclert A,

Dumas Milne Edwards J,

(GEST) GENSET 26-FEB-1999;

WPI; 2000-500381/45.

N-PSDB; AAC01122

21-FEB-2000; 2000EP-00200610.

06-SEP-2000.

99US-0122487P.

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0,
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a polypeptide encoded by one of a large number of 5. ESTB derived from mRNAs encoding secreted proteins. The 5. ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         claim 13; SEQ ID NO 5197; 71pp + Sequence Listing; English.
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4; Mismatches
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32 VEFIRHDR 39
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Matches

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1 XEFIXXDX 8

ò qq AAG01116 standard; protein; 69 AA.

RESULT 42 AAG01116

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Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                      New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                  present invention relates to proteins from Neisseria gonorrhoeae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori selected interacting domain (SID) protein #1236.
                                                                                                                                                                                                                                                                                                                                                                         ; Score 25; DB 6; Length 69; Pred. No. 1.1e+03; 4; Mismatches 0; Indels
                                                                                                            Masignani V, Monaci
                                                                                                                                                                                                         Disclosure, Page 325; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU51892 standard; protein; 72 AA.
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                                                                                                                                                                                                                                                                                                                                                                         100.0%;
50.0%; E
                                  12-FEB-2002; 2002WO-IB002069.
                                                            12-FEB-2001; 2001GB-00003424
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(INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QEFIGNDR 68
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                                                                                   (CHIR-) CHIRON SPA
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Best Local Similarity
                                                                                                                                               N-PSDB; ABZ38658.
                                                                                                                                                                                                                                                                                                                                                Sequence 69 AA;
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                                                                                                            Fontana MR,
            10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU51892
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New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing

ulcers in mammals

N-PSDB; ABX66637

Labigne A;

De Reuse H,

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Gaps

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                              The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see Table 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes substantially purified human proteins (referred to as open reading frame, OREX, where X is 1-11491 (see Tabl in the specification). ABN15762 to ABN2752 encode the human OREX proteins given in ABP00010 to ABP11500. OREX proteins are useful for treating or preventing a pathology associated with an OREX-associated
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                              Length 72;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                          Score 25; DB 5; L
Pred. No. 1.1e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ORFX protein sequence SEQ ID NO:18836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 18836; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AA.
 Claim 6; Page 386; 642pp; English
                                                                                                                                                                                                                    represent an illegible residue
                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP09427 standard; protein;
                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                    NEFIYADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABN25179
                                                                                                                                                                                                                                                        Sequence 72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP09427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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particularly of breast or prostate, or a genetic disease, in humans or

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Screening for non-ocular disease - by analysing tears for marker proteins, particularly indicative of cancer and genetic disease, also new proteins and nucleic acid encoding them.
disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with OREX-associated disorder. OREX polynucleotide sequences can be used in gene therapy. OREX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, Reloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rhemmatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The markers AAW61647-W61649 are used for screening for, or detecting, nor occular disease by analysing tears. Biochemicals, specifically proteins, are isolated from tears, particularly by chromatography or electrophoresis, especially two-dimensional polyacrylamide gel electrophoresis (2D-PAGE), then detected, e.g. with labelled specific reagents, in (radio)immunoassay. The method is used to detect cancer,
                                                                                                                                                                                                     arthritis, autoimmune thyroidists, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Score 25; DB 5; Length 73; Pred. No. 1.2e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; non-ocular disease; tear; cancer; breast; prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbert B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walsh B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW61649 standard; peptide; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 9; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-AU000071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-ocular disease marker 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MACQ-) MACQUARIE RES LTD. (UNIX ) UNISEARCH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willcox M, Bowilliams KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-447373/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LEFIPSDQ 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9835229-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998.
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Gooley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 46
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                                                                                                                                                                                                                                                                                                                                 epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                           0
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                                                               ; Score 25; DB 2; Length 74
Pred. No. 1.2e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 5; I 50.0%; Pred. No. 1.3e+03; iive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3004; 267pp; English
                                                                                                                                                                                                                         ABP38159 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00134001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0055779P
                                                                                                                                                                                                                                                                                                                                                     gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                   Query Match
Best Local Similarity 50...
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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QEFIDSDA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-381255/41.
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Matches 4; Conserv
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EEFINDDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 80 AA;
                                       AA;
                                                                                                                                                                                                                                                                                                                                       Staphylococcus
                                                                                                                                                                                                                                                                                                                                                      antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                             US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-1997;
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                                         74
                                                                                                                                                                                                                                                                               24-JUL-2002
                                                                                                                                                                                                                                                      ABP38159;
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                                         Seguence
             animals
                                                                                                                                                                                              RESULT 47
                                                                                                                                                                                                          ABP38159
ID ABP3
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RESULT

Molloy M;

ADA36717

us-09-660-302e-1.rag

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The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune chyroiditis;
                                                                                                                                                                                                                                                                                                     nucleotides - useful for developing prov
treatment of infections e.g. pneumonia
                                                                                                                                                                                          Lonetto MA, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 2; Length 82;
Pred. No. 1.3e+03;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX protein sequence SEQ ID NO:17204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae polynucleotides
                                                                                                                                                                                                                                                                                                                           for diagnosis, prevention and treatment
bacteremia, meningitis or endocarditis.
                                                                                                                                                                                          Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP08611 standard; protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 40; 181pp; English.
                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
50.0%; F
                                                         97WO-US021976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                        Hodgson JE,
Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                               WPI; 1998-322654/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : : | :
58 NEFIALDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myasthenia gravis.
                                                                                                                                                                                                                                                                   N-PSDB; AAV42950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200192523-A2
                                                       24-NOV-1997;
                                                                                             27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2002
                   04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2001.
                                                                                                                                                                                      Black MT,
                                                                                                                                                                                                            Reid RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP08611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated Acinetobacter baumannii nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 6; Length 80; Pred. No. 1.3e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; SEQ ID NO 8004; 328pp; English
                                                                                                                          Acinetobacter baumannii protein #3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae polypeptide
           ADA36717 standard; protein; 80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW62670 standard; protein; 82 AA
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                                                                                                                                                                                                                                                                                                                                                                            98US-0088701P
                                                                                                                                                                                                                                                                                                                                         99US-00328352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                        Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 DEFIFKDK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-576092/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-576092/
N-PSDB; ADA32591
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                       04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                          09-JUN-1998;
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                                                                                                                                                                                                                                                           US6562958-B1
                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                 13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW62670;
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Leach MD;

Shimkets RA,

WO9823631-A1

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Gaps

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98US-0093530P

21-JUL-1998;

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABD0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX associated disorder. ORFX polynucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arbitis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut transplants in the protection or regeneration and treatment of lung or liver form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp, wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aminoacyl-tRNA synthetase; isoleucyl-tRNA synthetase; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lysyl-tRNA synthetase; phenylalanyl-tRNA synthetase; gene expression;
prolyl-tRNA synthetase; herbicide identification; genetic marker;
plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice isoleucyl-RNA synthetase protein sequence.
                                                                                                                                                       Disclosure; SEQ ID NO 17204; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by NGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB83324 standard; protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00357251.
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62 REFICIDT 69
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Best Local Similarity
4; Conserve
              WPI; 2002-106308/14.
N-PSDB; ABN24363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1999;
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This sequence is a plant aminoacyl-tRNA synthetase of the invention. The aminoacyl-tRNA synthetases are selected from isoleucyl-tRNA synthetase, it lysyl-tRNA synthetase, phenylalanyl-tRNA synthetase, and prolyl-tRNA synthetase, phenylalanyl-tRNA synthetase, and prolyl-tRNA synthetase. The nucleic acid fragments may be used to create transgenic plants in which the polypeptides are present at higher or lower levels than normally found. This would have the effect of altering the level of aminoacyl-tRNA synthetase activity and gene expression in those cells. The polypeptides can be used as a targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. All or a substantial portion of the nucleic acid fragments may also be used as probes for genetically and physically mapping the genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                         Isolated polynuclectide encoding plant isolewcyl-LRNA synthase, useful for creating transgenic plants and as targets to facilitate design and/or identification of inhibitors that may be useful as herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice; isoleucyl-tRNA synthetase; lysyl-tRNA synthetase; phenylalanyl-tRNA synthetase; prolyl-tRNA synthetase; aminoacyl-tRNA synthetase; herbicide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice isoleucyl-tRNA synthetase clone rls2.pk0006.c10.
                                                           Orozco EM, Schwaber JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08739 standard; protein; 83 AA.
                                                                                                                                                                                                           Claim 1; Col 25-28; 50pp; English.
                             (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Unknown
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50.08; F
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99US-00357251.
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Best Local Similarity 50.0
Matches 4; Conservative
                                                             Famodu LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||::|:
31 EEFIFYDG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                            WPI; 2001-482449/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FALC/) FALCO S C. (FAMO/) FAMODU O O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 76
                                                                                                             N-PSDB; AAF87079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 83 AA;
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20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2003.
                                                             Falco SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 52
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9905-013963P

9905-0139817P

9905-0139817P

9905-0140635P

9905-0140635P

9905-0140635P

9905-0141242P

9905-0141242P

9905-0142055P

9905-0142055P

9905-014205P

9905-014284P

9905-014284P

9905-0144085P

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990S-013943P
990S-0139454P
990S-0139455P
990S-0139456P
990S-0139458P
990S-0139488P
990S-0139480P
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99US-013532P
99US-013622P
99US-013632P
99US-013632P
99US-013632P
                                                        99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0137502P.
99US-0137724P.
99US-0138094P.
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99US-0134219P.
99US-0134221P.
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                 99US-0132048P.
                                     99US-0132484P.
99US-0132485P.
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04 - JUN - 1
07 - JUN - 1
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24-MAY-1
25-MAY-1
27-MAY-1
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14-MAY-
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                                                                                      11-MAY
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                                                                                                                                                                                                          28-MAY
                                                                                                                                                                                                                     01-JUN
                                                                                                                                                                                                                                                                     NDC-01
                                                                                                                                                           20-MAY
The invention describes an isolated nucleic acid fragment encoding an isoleucyl-tRNA synthetase, a lysyl-tRNA synthetase, a phenylalanyl-tRNA synthetase. The nucleic acid fragments encoding aminoacyl-tRNA synthetases are useful in developing new herbicides that target aminoacyl-tRNA synthetases and engineer aminoacyl-tRNA synthetases and engineer aminoacyl-tRNA synthetases that are resistant to the herbicides. The nucleic acid fragments are also useful in facilitating studies to better understand protein synthesis in plants, providing genetic tools for the manipulation of gene expression, or providing possible target for herbicides. The polypeptides are useful as targets to facilitate design and/or identification of inhibitors of the aminoacyl-tRNA synthetases that may be used as herbicides. This is the aminoacyl-tRNA synthetases that may trNA synthetase clone r1s2.pk0006.c10
                                                                  New nucleic acid fragments encoding aminoacyl-tRNA synthetases, useful in developing new herbicides that target aminoacyl-tRNA synthetases and engineer aminoacyl-tRNA synthetases that are resistant to the herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 6; Length 83; 50.0%; Pred. No. 1.3e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 20148.
                   Simmons CR;
                                                                                                                                                                                                                                                                                                                                                                                                   AAG18654 standard; protein; 85 AA
                                                                                                          Claim 6; Page 15; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-01264P.
99US-01264P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-013077P.
99US-0130077P.
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                                                                                                                                                                                                                                                                                                            4; Conservative
                   Falco SC, Famodu 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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31 EEFIFYDG 38
(SIMM/) SIMMONS C R.
                                    WPI; 2003-401721/38.
N-PSDB; ABX95455.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                      Sequence 83 AA;
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05-MAR-1999;
09-MAR-1999;
03-MAR-1999;
25-MAR-1999;
01-APR-1999;
01-APR-1999;
08-APR-1999;
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19-APR-1999;
21-APR-1999;
23-APR-1999;
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9905-0147416P

9905-0147431P

9905-0148131P

9905-014864P

9905-0148665P

9905-0148665P

9905-0149368P

9905-0149368P

9905-0149308

9905-014930P

9905-014930P

9905-014930P

9905-0151066P

9905-0151066P

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990S-0154039P

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990S-015753P

990S-015763P

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990S-0159330P
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990S-0145218P
990S-0145918P
990S-0145919P
990S-0145918P
990S-0146388P
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99US-0145085P.
99US-0145087P.
99US-0145089P.
                                                99US-0145192P.
99US-0145145P.
99US-0145218P.
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                                 22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
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02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
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13-AUG-1999)
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25-AUG-1999)
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30-AUG-1999;
31-AUG-1999;
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23-SEP-1999;
24-SEP-1999;
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14-OCT-1999;
14-OCT-1999;
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12-AUG-1999;
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
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                                                                                                                                                                                                                                                              100.0%; Score 25; DB 3; Length 85; 50.0%; Pred. No. 1.4e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 24; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herbicidally active polypeptide SEQ ID NO 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                             ABB90813 standard; protein; 89 AA
        9905-0159584P-
9905-0160741P-
9905-016076P-
9905-016070P-
9905-016081P-
9905-0160981P-
9905-0160981P-
9905-016196P-
9905-016196P-
9905-0161361P-
9905-0161361P-
9905-0161361P-
9905-0161361P-
9905-0161361P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tietjen K, Weidler M;
                                                                                                                                                                                                                                                                                                                            :|||::|:
13 PEFIFEDG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                             1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200210210-A2.
                                21-OCT-1999
21-OCT-1999
21-OCT-1999
22-OCT-1999
22-OCT-1999
22-OCT-1999
25-OCT-1999
25-OCT-1999
26-OCT-1999
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26-OCT-1999
28-OCT-1999
28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABB90813;
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                        RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                   ABB90813
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cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                         Human, open reading frame, ORFX, gene therapy, cancer, cirrhosis, hyperproliferative disorder, psoriasis, benign tumour, haemorrhage, degenerative disorder, osteoarthritis, neurodegenerative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 15438; 1037pp; English.
                                                                                    Human ORFX protein sequence SEQ ID NO:15438.
                     ABP07728 standard; protein; 94 AA.
                                                                                                                                                                                                                                                                                                30-MAY-2000; 2000US-0206132P.
                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US010836
                                                                                                                                                                                                                                                                                                          29-AUG-2000; 2000US-0228716P
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                     Leach
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106308/14.
                                                                                                                                                                                      myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABN23480
                                                                                                                                                                                                                                WO200192523-A2
                                                                                                                                                                                                                                                                                                                                                       RA,
                                                                                                                                                                                                           sapiens.
                                                                25-JUN-2002
                                                                                                                                                                                                                                                     06-DEC-2001
                                          ABP07728;
                                                                                                                                                                                                                                                                                                                                                       Shimkets
                                                                                                                                                                                                            Homo
RESULT 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human relaxin may be prepd. by combining the A and B chains of relaxin in full-length, shortened or modified forms. Prefd. analogues consist of any one of the A-chains A(1-24), A(2-24), A(3-24) in combination with any of the B-chains B(1-23) to B(1-32). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uman relaxin analogues - has shortened and/or modified forms of natural and/or A chains modified by addn. of protective gp. to free amino gp.
                                                                            Gaps
 identifying modulators. The identified modulators are useful as
                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 90;
                                                     Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 25; DB 1; Length 90 Pred. No. 1.4e+03; 4; Mismatches 0; Indels
                                           Score 25; DB 5,
-4 No. 1.4e+03; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tregear GW;
                                                                Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                                                                                                           Hormone; relaxin analogue; antagonist
                                                                                                                                                                                                                                                     Sequence of human prorelaxin B chain.
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2B; 22pp; English.
                                                                                                                                                                           AAP81887 standard; protein; 90 AA
                                                                                                                                                                                                                                                                                                                                                                 /label= C PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niall HD,
                                                                                                                                                                                                                                                                                                                                           'label= B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                  83EP-00104503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       82AU-00005352.
88EP-00104503.
                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                50.08;
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                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0-
                                                                            Conservative
                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shine J,
                                                                                                            :|||::|:
52 TEFIRSDI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-300910/43.
                                                                                                 1 XEFIXXDX 8
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN81773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90 AA;
                                  Sequence 89 AA;
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1982;
23-APR-1987;
                                                                                                                                                                                                                                31-DEC-1990
                                                                             4;
                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                       EP287820-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hudson PJ,
           herbicides
                                                                                                                                                                                                 AAP81887;
                                                                                                                                                                                                                                                                                                                                                       Peptide
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27522 encode the human ORFX in the specification). ABN15762 to ABN27522 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squances can be used in gene therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, comparise, bening tumnours, kebloid, degenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic storage disease, various immune deficiencies and disorders, intertious diseases, autoimmune thyroiditis, myasthenia gravis, rheumatoid attention autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut compared or systemic cytokine damage. N.B. The sequence data for this patent did not form after the printed specification, but was obtained in electronic formers of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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Pred. No. 1.5e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; I
Matches 4; Conservative 4;
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Gaps

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1 XEFIXXDX 8

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This sequence comprises human endometrial specific steroid binding factor III (ESF III), a protein that inhibits phospholipase A2 activity, binds to polychlorinated biphenyl compounds, reduces foreign protein antigenicity, inhibits monocyte and neutrophil chemotaxis and phagocytosis, inhibits monocyte and neutrophil chemotaxis and controls the growth of endometrial cells. The amino acid sequence was deduced from a CDNA clone (see AAT94832) derived from a human endometrial tumour. ESF I (see AAW35802) and ESF II (see AAW35802) and ESF II (see CAAF98832) and ESF II II (see CAAF98832) and ESF II II or III (including expression of the ESF II II or III (including expression of the CAFF III or III (including expression of the ESF polypeptide. hESF II and III may be used the continual continual continual continual children in vivo) and (b) for identifying compounds which bind to and inhibit activation of the ESF polypeptide. hESF II II and III may be used to the ESF polypeptide. hESF II II and III may disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human endometrial specific steroid-binding factor I, II and III - used to treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endometrial specific steroid-binding factor III; ESF III; human; Clara cell secretory protein; endometrium; phospholipase A2 inhibitor; polychlorinated biphenyl; antiaggregant; inflammation; asthma; rhinitis; cystic fibrosis; airway disease; neoplasia; atopy; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human endometrial specific steroid-binding factor III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .21
/label= Sig_peptide
22. .95
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                           AAW35804 standard; protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US003857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US003857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentz RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasia, atopy etc.
                                                                     47 PEFIEVDL 54
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XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9734997-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                     AAW35804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                             RESULT 57
                                                                                                                                                                                                                                      AAW35804
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The present sequence represents a human mammoglobin homologue (HWH).
Antagonists of the HMH polypeptide can be used to treat neoplastic
disorders including adenocarcinoma, leukemia, lymphona, melanoma,
myeloma, sarcoma and teratocarcinoma. A vector expressing the complement
of the polymucleotide encoding HMH may be administered to a subject to
treat or prevent neoplastic disorders or endometriosis. Antibodise which
bind HMH may also be used in the disorders of conditions or diseases
claracterized by expression of HMH, or in assays to monitor patients
being treated with HMH, agonists, antagonists or inhibitors.
Cobyructeotides encoding HMH may also be used diagnostically to detect
and quantitate gene expression in biopsied tissues. With respect to
cancer a relatively high amount of transcript may indicate a
predisposition for the development of disease. The nucleic acid sequences
which encode HMH may also be used to generate hybridization probes useful
for mapping the naturally occurring genomic sequence. HMH, and its
fragments/variants can be used for screening libraries of compounds in
drug screening techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human mammoglobin homolog (HMH), useful for diagnosing, treating or preventing disorders associated with expression of HMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                      Human manmoglobin homologue, HMH; antagonist; neoplastic disorder;
adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;
teratocarcinoma; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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50.0%; Pred. No. 1.5e+03;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                      A human mammoglobin homologue (HMH).
                                                                                                                    AAY02590 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB03769 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1A-B; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murry LE;
                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US021729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00951750.
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
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47 QEFIDSDA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           WO9919487-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1997;
                                                                                                                                                                                      26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman JL,
                                                                                                                                                      AAY02590;
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Matches
                                                                                    RESULT 58
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ID AAB0
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Gaps .,

100.0%; Score 25; DB 2; Length 95; larity 50.0%; Pred. No. 1.5e+03; Conservative 4; Mismatches 0; Indels

Best Local Similarity Matches 4: Conserve

Query Match

(first entry)

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Human endometrial specific steroid-binding factor III protein sequence.
                                                                                                                                            Claim 1; Fig 3; 36pp; English
                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                    Gentz R, Ni J;
                                                                                                             WPI; 2000-375600/32.
                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conserv
                                                                                                                 N-PSDB; AAA59730
                                                                                                                                                                                                                                                               Sequence 95 AA;
            06-OCT-2000
                                                Homo sapiens
                                                                          21-MAR-1997;
                                                                                   21-MAR-1996;
                                                        US6066724-A
                                                                 23-MAY-2000
                                                                                                                                                                                                                                                                       Query Match
    AAB03769;
                                                                                                    Yu G,
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96US-0014724P. 97US-00821451.

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sequences, corresponding to human secreted proteins. AAY4651 to AAY5438 sequences, corresponding to human secreted proteins. AAY4651 to AAY5438 represent the EST-related proteins corresponding to AAZ42265 to AAZ43052.

The 5. BSTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromssome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals per consist of indiance acids encoding signal peptides can be used in gene therapy protocols. The cucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a collypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins la valueble. AAZ42249 to AAZ42264 and AAX64644 to AAX6650 represent sequences used in the exemplification
                                                                                                                 Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
location; development; protein synthesis; stability; regulation;
identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                              Human 5' EST related polypeptide SEQ ID NO:1555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 818; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY92226 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
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                                                  01-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBFIDSDA 54
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEST ) GENSET
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                             WO9953051-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1999;
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AAY65394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY92226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to nucleic acid molecules encoding portions of the human endometrial specific steroid-binding factors I, II, and III. Also included in the invention are hESF I, II, and III polypeptide sequences. The included in the invention are hESF I, II, and III polypeptides sequences. The included in the invention are hESF I, III and III polypeptides are used in gene therapy to express hESF I, II and III polypeptides in vivo to treat and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way disease, neoplasia and actory. The polymuclectides are also used to inhibit phospholipase A2 activity, bind polychorinate block to inhibit phospholipase A2 activity, bind polychorinate elosation of inhibit phospholipase A2 activity, inhibit monocyte and neutrophil chemotaxis and phagocytosis, inhibit platelet aggregation, regulate elosatoid cand phagocytosis, inhibit platelet aggregation, regulate elosatoid cand phagocytosis, inhibit platelet aggregation, regulate elosatoid con polymucleotides are also useful for detecting complementary colling phymoleotides are also useful for detecting complementary polymucleotides are used to detect complementary polymucleotides such as associated with a dysfunction will provide a diagnostic tool that can define diagnosis of a disease or susceptibility to a disease which can be the from under-expression, over-expression of a commetrial cancer. They are also useful for chromosome identification.
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0
                                                                                                                                                                               Endometrial specific steroid-binding factor; human; hESF; inflammation; asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy; eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel gene encoding human endometrial specific steroid-binding factor I, II and III which is useful for treating asthma, rhinitis, cystic fibrosis, airway disease and neoplasia.
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100.0%; Score 25; DB 3; Length 95; 50.0%; Pred. No. 1.5e+03; ive 4; Mismatches 0; Indels

Conservative

1 XEFIXXDX 8

QEFIDSDA

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AAY65394 standard; protein; 95 AA.

RESULT 60 AAY65394 ID AAY65 XX

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                           Alzheimer's and atherosclerosis.
                                                                                                               Claim 23; Fig 6; 118pp; English
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                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                      100.08;
50.08; F
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97US-00821451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                              AAB31682 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                          Conservative
     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                               54
                                           2000-303741/26.
                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                               47 QEFIDSDA
                                                   N-PSDB; AAA09118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF25214.
                                                                                                                                                                                                                                 Sequence 95 AA;
                                                                                   cytokine-like
                      Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6174992-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2001
                                                                                                                                                                                                              skeletal
                                                                                                                                                                                                                                                                                                                                                                                   AAB31682;
                                                                      Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                    The levels of human endometrial specific steroid binding factor (ESBPIII) can be measured and compared to control levels and used to diagnose the presence of a gynaecological (uterine, breast, endometrial, or ovarian) cancer in a patient. ESBPIII levels can also be used to diagnose metastasis, to stage or monitor gynaecological cancer. Antibodies specific for ESBPIII can be used to treat gynecological cancers
                                                                                                                                                                                                                                       staging and monitoring gynecological cancer comprising using level of ESBPIII in a patient as an indicator of cancer.
                            Endometrial specific steroid binding factor; ESBPIII; diagnosis;
gynaecological cancer; uterine; breast; endometrial; ovarian; antibody;
gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone Mamm-X; mammaglobin; breast cancer; cytostatic; anti-HIV; immunosuppressive; antiallergic; antiinfective; antiinflammatory; antiarthritic; antiateriosclerotic; vasotropic; neuroprotective; nootropic; dermatological; tranquilizer; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 3; Length 95; 50.0%; Pred. No. 1.5e+03; ive 4; Mismatches 0; Indels
         Human endometrial specific steroid binding factor III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammoglobin homologue from clone Mamm-X.
                                                                                                                                                                                                                                                                   Claim 6; Page 28-29; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY92237 standard; protein; 95 AA.
                                                                                                                              99WO-US022753
                                                                                                                                                 98US-0102743P
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99US-00412231
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                  (DIAD-) DIADEXUS LLC.
                                                                                                                                                                                                         2000-303649/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                        QEFIDSDA 54
                                                                                                                                                                                                                                                                                                                                                                                                                    1 XEFIXXDX 8
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les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                           95 AA;
                                                                                      WO200020044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200020447-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone Mamm-X;
                                                                    Homo sapiens.
                                                                                                                             30-SEP-1999;
                                                                                                                                                02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-2000
                                                                                                                                                                                                                                       Diagnosing,
an elevated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-1998;
                                                                                                         13-APR-2000
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                                                                                                                                                                                      Macina RA;
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Best Local S:
Matches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY92237;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 62
qq
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Clone Mamm-X encodes a polypeptide that is 100 pecent identical to human Mammaglobin B precursor, a potential marker of breast cancer nodal metastasis. The sequences are useful for treatment of diseases such as cancer, immune disorders, autoimmune disease, acquired immune deficiency syndrome (AIDS), transplant rejection, allergy, infection by a pathological agent or organism, inflammarory disorders, arthritis, a haematopoietic disorder, a skin disorder, alberosclerosis, restenosis, a neurological disease, Alzheimer's disease, trauma, spinal cord injury and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, endometrial specific steroid binding factor, hESF, hESF1; hESFII; hESFIII; inflammation; asthma; rhinitis, cystic fibrosis, airway disease, neoplasia, atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis; phagocytosis; platelet aggregation; eicosanoid; endometrial cell.
acids encoding polypeptides with syncline-like, claudin-like or a-like activity, useful for treating diseases including cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human endometrial specific steroid binding factors, useful for treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 3;
Pred. No. 1.5e+03;
4; Mismatches 0;
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/note= "signal peptide"
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invention

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                                                        The present sequence represents a human endometrial specific steroid hinding factor (hESF). The specification describes hESFI, hESFII, and hESFIII. I and III polypeptides, and polymucleotides encoding them are useful for treating and preventing inflammation, asthma, rhinitis, cystic fibrosis, airway disease, neoplasia and atopy, inhibiting phospholipase A2 activity, binding polychlorinated biphenyls, reducing foreign protein antigentity, inhibiting monocyte and neutrophil chemotaxis and phagocytosis, inhibiting platelet aggregation, regulating encommental levels in the human uterus, and for controlling the growth of endometrial cells. hESF polypeptides and nucleotides are also useful for research, biological, clinical or therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides having the sequence of human lipophilin A, B and C are associated with carcinomas of hormonally regulated organs and are useful
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic epitope; hormonally regulated organ; malignant tumour;
Lipophilin; human.
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                                                                                                                                                                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                         Score 25; DB 4; Length 95
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the diagnosis and prognosis of various cancers.
 airway disease, neoplasia and atopy.
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                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO20555 standard; protein; 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein of human Lipophilin C.
                                 Claim 1; Fig 3; 36pp; English
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                                                                                                                                                                                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                           Conservative
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OEFIDSDA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLASGOW B J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-338922/37
                                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                              Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 64
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                                                                                                                                                                                                                                                                                                                                  Human; ovarian cancer, marker, cancer, familial history, brain disorder, central nervous system disorder, bacterial meningitis; viral meningitis; Alzheimer's disease, Parkinson's disease, cerebral oedema, hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kovatis SG;
                                                            0
                          Length 95;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gannavarapu M, Hoersch S, Kamatkar S, Ko
Morrisey MP, Olandt PJ, Sen A, Vieby PO,
1 K, Schmandt RE, Zhao X, Glatt K;
                          Score 25; DB 5; L
Pred. No. 1.5e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 303; 481pp; English.
                                                                                                                                                                                                          95 AA
                                                                                                                                                                                                                                                                                                        Human ovarian cancer marker M458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0276025P.
2001US-0276026P.
2001US-0311732P.
2001US-0323580P.
                            100.0%;
50.0%; I
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2001US-0325102P.
2001US-0325149P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                          ABG96366 standard; protein;
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a non cancer patient
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-723277/78.
                                                                                                                           54
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                              Query Match
Best Local Similarity
                                                                                                               :|||::|:
47 QEFIDSDA
                                                                                            1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABS76462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu K,
Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200271928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2001;
14-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-2001;
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26-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2002
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Bast RC,
                                                                                                                                                                                                                                          ABG96366;
                                                              Matches
                                                                                                                                                                             RESULT 65
                                                                                                                                                                                              ABG96366
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                                                                           testicular disorders (e.g. nontuberculous granulomatcus orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the
             of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody specific for human endometrial specific steroid-binding factor (hESF) III, useful for detecting hESF III protein in biological sample and to isolate or identify clones expressing the protein.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, endometrial specific steroid-binding factor; BSF;
prostatic steroid-binding protein; hBSF I; hESF II; hBSF III; asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human endometrial specific steroid-binding factor (hESF) III.
                                                                                                                                                                                                                                                                                                Score 25; DB 5; Length 95;
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
The cancer markers may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22. .95
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .21
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                 100.0%;
50.0%; I
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99US-00263810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0014724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                              1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                      Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6338948-B1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-1996;
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08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB09635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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The present sequence represents a endometrial specific steroid-binding

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factor (hESF) III. The full length protein has a molecular weight of 8.10 KDB. The protein has homology to rat protein seteroid-binding protein C3. Antibodies which bind hESF proteins, such as hESF I, hESF II, and hESF III are useful for isolating or to identify clones expressing the bolypeptides or to purify the polypeptides by affinity chromatography. Agonists and antagonists of hESF proteins are useful for treating and/or preventing susceptibility to asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endometrial specific steroid-binding factors 1, II and III (hESF I, II and III) (hESF I, III and III) (hESF I, II and III) (hESF III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rial specific steroid-binding factor (hESF) proteins and treating or diagnosing a disease or susceptibility to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human endometrial specific steroid-binding factor III (hESF III) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, endometrial specific steroid-binding factor; hESF;
Clara cell 10 kDa, CC10, secretory protein; asthma;
prostatic steroid-binding protein; hormone; lung; uterus; gene therapy
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses isolated polypeptides, which comprise human
                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                      Length 95;
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Pred. No. 1.5e+03;
1; Mismatches 0;
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|label= Signal_peptide
| 2. .95
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                                                                                                                                                                                                                                                                 100.0%;
50.0%; F
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99US-00263810.
2000US-00583169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 50.0.
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eful for tres
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OEFIDSDA 54
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                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                Sequence 95
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                                                                                                                                                                                                                                                                                                                                                                                                                      47
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ABP01586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
or develop antagonists against the isolated hESF polypeptide. The polypeptides or polymuclectides are useful for treating a patient having a need of hESF I, hESF III or for treating a patient having an eneed to inhibit hESF. The polypeptide is administered by providing to the patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In patients, the disease is asthma. The hESF polypeptides or polymuclectides are also useful for diagnosing a disease or a susceptibility to the disease. The sequence presented is the hESF III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meyers RE;
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers R
Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breast cancer diagnosis or treatment by comparing the level of expr
of a marker in a patient sample with that in the control non-breast
cancer sample.
                                                                                                                                                                                  0;
                                                                                                                                           Score 25; DB 6; Lengtn >2,
Pred, No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                            Breast cancer associated protein sequence SEQ ID NO:280.
                                                                                                                                                                                                                                                                                                                                                                                                     Human; breast cancer; cytostatic; gene therapy
                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                   ABR47522 standard; protein; 95 AA.
                                                                                                                                                          100.08;
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18-JUL-2001; 2001US-030561LP.
2-SEP-2001; 2001US-0325002P.
05-MAR-2002; 2002US-0352585P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2002; 2002WO-US019669.
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                                                                                                                                                                   50.0%;
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                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                           1 XEFIXXDX 8
                                                                                                                                                                      Local Similarity
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                                                                                                                                  Sequence 95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polynuclectide and polypeptide, useful for the manufacture of a medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; PRO; cancer; inflammatory bowel disease; ulcerative colitis; Crohn's disease.
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                                                                                                                                Length 95;
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                                                                                                                                                                         Indels
                                                                                                                             Score 25; DB 6; L. Pred. No. 1.5e+03; 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 7; L
Pred. No. 1.5e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; SEQ ID NO 24; 327pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP01586 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                     ADC78795 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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50.0%; E
                                                                                                                                100.0%;
50.0%; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO protein #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-481990/45.
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QEFIDSDA 54
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                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                              : | | | : : | : 47 QEFIDSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 XEFIXXDX
                                                                                                                                                                                                                      1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003034984-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 95 AA;
                                                                                          Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                             ADC78795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                           RESULT 69
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(CURA-) CURAGEN CORP.
                                                             2002-106308/14.
                         myasthenia gravis.
                                                                N-PSDB; ABN17338.
                                 WO200192523-A2.
                                                                                                                                      Sequence 97 AA;
                             Homo sapiens.
                                                         Shimkets RA,
  25-JUN-2002
                                      06-DEC-2001.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 16920; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheat; aspartyl-tRNA synthetase; herbicide; genetic mapping; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 4; Length 98; 50.0%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat aspartyl-tRNA synthetase from clone wleln.pk0021.e6.
                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 16920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.6e
4; Mismatches
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                                                                    ABB63376 standard; protein; 98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US009231.
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2000US-00614150.
                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL07479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions.
                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
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                                                                                                                               ABB63376;
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         RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE03588
                                        ABB6337(
                                                                                                                            XXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABN15762 to ABN27525 encode the human ORFX of in the specification). ABN15762 to ABN27525 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorders or be used in the threapy. ORFX sequences can be used in the threapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, or portiant of cancer, hyperproliferative disorders, disorders and interpretation cardiovascular diseases, disorders mallitus, systemic contrary at the contrary of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                            hyperproliferative disorder; psoriasis; benign tumour; haemorrhage, degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; ollesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did no form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/pub/sublished pot sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                         frame, ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3154; 1037pp; English.
                                                           Human ORFX protein sequence SEQ ID NO:3154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000US-0206132P, 29-AUG-2000; 2000US-0228716P.
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(first entry)
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0; Indels

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53

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Query Match Best Local Similarity

Matches

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99US - 0134256P

99US - 013421BP

99US - 013421BP

99US - 0134370P

99US - 0134341P

99US - 0135134P

99US - 0135134P

99US - 0135134P

99US - 013522P

99US - 013632P

99US - 0137744P

99US - 013734P

99US - 013943P

99US - 013943P

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99US - 0139453P

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99US - 0139455P
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99US-013946DP.
99US-013946ZP.
99US-013946ZP.
99US-013976ZP.
99US-013976ZP.
99US-013976ZP.
99US-01398ZP.
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99US-0140695P.
99US-0140823P.
99US-0140991P.
99US-0141842P.
99US-0141842P.
99US-0128234P.
99US-0128714P.
99US-012945P.
99US-0130449P.
99US-0130510P.
99US-0130810P.
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99US-0142390P.
99US-0142803P.
99US-0142920P.
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99US-0143542P.
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99US-0144325P.
99US-0144331P.
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23-APR-1999;
28-APR-1999;
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-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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22-JUN-1999;
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03-JUN-1999
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05-MAY-1999
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06-MAY-1999
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08-JUN-19
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                                                                                                                                                                                                                  MAY-
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                                                                                                                                                                                                                                    The present sequence is wheat aspartyl-tRNA synthetase of the invention. The aspartyl-tRNA synthetase are used as targets to facilitate designing and identification of inhibitors of the enzymes which are useful as herbicides. All or a substantial portion of the nucleic acid fragments of the present invention are used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information is useful in plant breeding in order to develop lines with desired phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                           New isolated polynucleotide encoding an aspartyl-tRNA synthetase useful as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                             ; Score 25; DB 4; Length 98; Pred. No. 1.6e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 41798.
                                                                                                                             Rafalski JA;
                                                                                                                                                                                                                  Claim 12; Col 33-36; 40pp; English.
                                                                                                М
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG34364 standard; protein; 99 AA.
                                                                                               (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                             100.0%;
50.0%; P
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126784P.
99US-0126785P.
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                                                          99US-00352990
                                                                            98US-0092866P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                             Famodu LO, Orozco EM,
                                                                                                                                                                                                                                                                                                                                                                                               : | | | :: | :
CEFIGLDA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                               WPI; 2001-388927/41.
                                                                                                                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
  Triticum aestivum.
                                                                                                                                                          N-PSDB; AAD07972
                                                                                                                                                                                                                                                                                                                            Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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                                                          14-JUL-1999;
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                    US6255090-B1
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                                      03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG34364;
                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 73
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99US-0144332P. 99US-0144333P. 99US-0144333P. 99US-0144333P. 99US-0144333P. 99US-0144333P. 99US-0144632P. 99US-0144632P. 99US-014608P. 99US-014608P. 99US-014508P. 99US-014508P. 99US-014508P. 99US-014508P. 99US-0145218P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014528P. 99US-014538P. 99US-0147303P. 99US-014733P. 99US-014733P. 99US-014936P. 99US-014938P. 99US-014938P. 99US-014938P. 99US-014938P. 99US-014938P. 99US-0151065P. 99US-0151065P. 99US-0151065P. 99US-0151065P. 99US-0151065P.	0.03 - 0.15 - 0.
19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 25-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28	
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Acinetobacter baumannii, bacterial disease, antibacterial, vaccine, plant biocontrol agent.
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                               Length 99;
                                                                                                                                                                                                                                                              h Sore 25; DB 3; Length 99 Similarity 50.0%; Pred. No. 1.6e+03; 4; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter baumannii protein #3608.
                                                                                                                                                                                                                                                                                                                                                                 ADA36447 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
990S-0159294P.
990S-0159329P.
990S-0159331P.
990S-0159631P.
990S-0159638P.
990S-0169638P.
990S-016076P.
990S-016081SP.
990S-016081SP.
990S-016080P.
990S-0160980P.
990S-0160980P.
990S-0160980P.
990S-0160980P.
990S-0160980P.
                                                                                                                                                                                                      990XS-0161361P.
990XS-0161920P.
990XS-0161992P.
990XS-0161993P.
990XS-0162142P.
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                             :|||::|:
46 QEFIVDDL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-576092/54.
N-PSDB; ADA32321.
                                                                                                                                                                                                                                                                                                  1 XEFIXXDX 8
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breton G, Bush D;
       13-0CT-1999)
14-0CT-1999)
14-0CT-1999)
14-0CT-1999)
14-0CT-1999)
                                                                                         21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                               18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6562958-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .89-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                   ADA36447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants.
                                                                                                                                                                                                                                                                                                                                               RESULT 74
ADA36447
à
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Example; SEQ ID NO 7734; 328pp; English

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      The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagonosing a bacterial disease, as components of antibacterial vaccines, as targets for anibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Arabidopsis genes - useful for producing transgenic plants which show resistance to cell death caused by pathogens or herbicides.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of LSD1-interacting protein 00 of
                                                                                                                                                                                                                                                                                                                                                                                                                       LSD1-interacting protein OO; plant pathogen response; apoptosis; programmed cell death; disease resistance; herbicide resistance; transgenic plant; crop protection.
                                                                                                                                                                                              0
                                                                                                                                                                    Length 99;
                                                                                                                                                                   Score 25; DB 6; Length 99
Pred. No. 1.6e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Pathogen response protein LSD1-interacting protein 00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epple PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dietrich RA, Richberg MH,
                                                                                                                                                                                                                                                                                                                AAW72393 standard; protein; 101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 46; Page 65; 88pp; English.
                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US004077.
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                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                38 PEFIVKDK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-531501/45.
                                                                                                                                                                                                                       1 XEFIXXDX 8
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                                                                                                                                           Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9837755-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                           AAW72393;
                                                                                                                                                                                                                                                                                      RESULT 75
                                                                                                                                                                                                                                                                                                     AAW72393
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Arabidopsis thaliana. LSD1 interacting genes (see AAV66755-67) were isolated from a yeast gene expression library constructed in plasmid pJG4 solated from Arabidopsis leaves infected with Pseudomonas syringae. A two-hybrid system was used with LSD1 short and long open reading frames (see AAV66750-51) as bait. LSD1 (see AAW7236-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Since the inactivation of LSD1 by mutation leads to enhanced disease resistance, enhanced resistance to pathogens. Thus, the invention includes all proteins (see AAW72384-96) that interact with the cell death regulator

Sequence 101 AA;

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ABN79587 represent cDNAs encoding them. The invention also encompasses
polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynucleotides at least 85% identical to
the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
polynucleotides, the recombinant production of ORFX proteins, antibodies
specific for ORFX proteins, methods of detecting ORFX polynucleotides and
activity, and methods of screening for modulators of ORFX expression or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
cange of biological activities, such as cytokine, cell proliferation,
cell differentiation, immune modulation, hematopoiesis regulation,
tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
chemokinetic activity, haemostatic activity, thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; entropedetive; antidiabetic; cytostatic; nootropic; cardiant; hypotensive; antidiaptycid; antidialmatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ORF; open reading frame; ORFX; drug screening; diagnosis; implicated ontitoring; oytokine; cell proliferation; cell differentiation; immune modulation; haematopoies regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; mente system disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                .
Score 25; DB 2; Lengu...
No. 1.6e+03;
0; Indels
                                    Length 101;
                                                          Pred. No. 1.6e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Human ORF1675 protein, SEQ ID NO:3350.
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                                                                                                                                                                                                                                                                       ABP32702 standard; protein; 103 AA.
                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2001; 2001WO-US017076.
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                                                            50.08;
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                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leach MD, Shimkets RA;
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                                                                                                                                                                IEFICLDL 82
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                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                         1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       08-JUL-2002
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cc receptor/ligand, antinflammatory activity, tumour inhibition activity, and antinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OFEX proteins, concluded antibodies may be used in the treatment of cancers, concluded actions and antibodies may be used in the treatment of cancers, concluded antibodies may be used in the treatment of cancers, conterns such as peoriasis and benign tumours, conterns and disorders such as peoriasis and Alaheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage diseases, and infectious diseases caused by viral, bacterial, chungal and other pathogens. OREX uncleic acids may also be used as a source of primers and probes, in the detection of OREX genomic sequences or transcripts, in the identification and cloning of homologous contensorables, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The OREX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of OREX protein, and in drug screening. The OREX proteins may also be used as immunogens to generate specific antibodies, which are useful in the content and monitoring of OREX-associated diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic, Anti-inflammatory, Osteopathic; Neuroprotective, Nootropic, Gene Therapy, human, secretory protein, membrane proteins, cancer, inflammatory disease, osteoporosis, neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii S;
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<, Irie R,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 5; Length 103;
Pred. No. 1.7e+03;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.7e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 2020; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA54452 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELL-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
50.0%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002EP-00006586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein, SEQ ID 2020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J, Isono Y,
Yoshikawa T,
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29 GEFIEGDK 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amamoto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA54452;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The present invention relates to novel human secretory or membrane

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immunosuppressive; antiînflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                             Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                Gaps
proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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0
                                                               Score 25; DB 6; Leng...
No. 1.7e+03; No. 1.7e+63; O; Indels
                                                                                        Length 105;
                                                                                                                                                                                                                                                                                                   Human nervous system related polypeptide SEQ ID NO 6027.
                                                                                                   Pred. No. 1.76
                                                                                                                                                                                                                          ABB17370 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0179065P.
2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
                                                                                       100.0%;
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2000US-0209467P.
2000US-0214886P.
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2000US-0216647P.
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2000US-0198123P.
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2000US-0217496P.
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                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                4; Conservative
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4 EEFIFYDY 11
                                                                                                                                       1 XEFIXXDX 8
                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                               Sequence 105 AA;
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16-MAR-2000;
17-MAR-2000;
19-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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07-JUL-2000;
07-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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11-JUL-2000;
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ABB17370
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02 - OCT - 2000; 20000S - 0226802P; 02 - OCT - 2000; 20000S - 0226802P; 02 - OCT - 2000; 20000S - 023703P; 02 - OCT - 2000; 20000S - 023703P; 02 - OCT - 2000; 20000S - 023703P; 03 - OCT - 2000; 20000S - 023993F; 13 - OCT - 2000; 20000S - 02499F; 13 - OCT - 2000; 20000S - 024178F; 20 - OCT - 2000; 20000S - 024178F; 20 - OCT - 2000; 20000S - 024178F; 20 - OCT - 2000; 20000S - 024186P; 20 - OCT - 2000; 20000S - 024647F; 20 - OCT - 2000; 20000S - 024652F; 20 - OCT - 2000S - 024652F; 20 - OCT - 2000S - 024652F; 20 - OCT - 2000S - 0246552F; 2000S - 024652F; 20 - OCT - 2000S - 024652F; 20 - OCT - 2000S - 024652F; 20 - OCT - 2000S -
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-02216868P.
23-AUG-2000; 2000US-02216868P.
23-AUG-2000; 2000US-022294P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229344P.
06-SEP-2000; 2000US-0229344P.
06-SEP-2000; 2000US-0229343P.
06-SEP-2000; 2000US-0229343P.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-02393P.
06-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023196P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-02333064P.
14-SEP-2000; 2000US-0233364P.
25-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
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27-SEP-2000; 200
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB146'08-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) cinfections diseases such as viral, bacterial, fungal and parasitic infections between the sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system antigen polypeptides, and/or treating nervous system cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 6027; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 3224 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Barash SC, Ruben SM;
2000US-0249207P

2000US-0249209P

2000US-0249211P

2000US-0249211P

2000US-0249211P

2000US-0249213P

2000US-0249213P

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2000US-024924P

2000US-024924P

2000US-024929P

2000US-0250391P

2000US-0251391P

2000US-0251391P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; ABA13696.
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                                                                                                                                                                                                                                                                          117-NOV-2000; 2
117-NOV-2000; 2
117-NOV-2000; 2
117-NOV-2000; 2
01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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Gaps

·: 0

100.0%; Score 25; DB 4; Length 106; 50.0%; Pred. No. 1.7e+03; tive 4; Mismatches 0; Indels

4; Conservative

Best Local Similarity Matches 4; Conserv

Query Match

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1 XEFIXXDX 8

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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide reductases) appearing as ABUS8184 ABUS81846 (or a protein 80% identical to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included are expression cassettes, transformed host cells, transgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor.
                                                                                                                                  Plant; EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odell JT,
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            ABU58228 standard; protein; 106 AA.
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                                                                                                     Wheat stress response protein #18.
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Weng Z;
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99US-0133042P.
99US-0133427P.
99US-0133428P.
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99US-0137667P.
2000US-00566394.
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                                                                        (first entry)
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ODELL J T.
RAFALSKI J A.
THORPE C J.
SAKAI H.
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Sakai H,
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FAMODU O O.
MEYERS B C.
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                                                                                                                                                                                                           Triticum aestivum.
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N-PSDB; ABX78399.
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                                          ABU58228;
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(MEYE/)
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ABU58228
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Enterococcus facetum encoding an Enterococcus facetum polypeptide

Enterococcus facetum encoding an Enterococcus facetum polypeptide

Composition of 10 fully defined sequences given in the (or comprising 40

Sequential nucleotides chosen from any of the nucleic acids, its

complement or sequences hybridising to it. Also included are a

complement vector comprising the nucleic acid operably linked to

transcription regulatory element, a cell comprising the vector and a

single-stranded probe comprising the nucleic acid. The nucleic acids are

chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.

The nucleic acids is useful for diagnosting pathological conditions

resulting from E. faectum bacterial infection (e.g. urinary tract

infection, bacteraemia, endocarditis, wounds and abdominal-pelvic

infection, and for secrening drugs such as agonists and antagonists. The

nucleic acid is useful for recombinant production of Candida albicans -

derived peptides or antisense polypeptides. Pharmaceutical compositions

and vascoines containing the nucleic acid are useful for preventing or

treating Enterococcus faecium infections. The present sequence represents

one if the disclosed E. faecium proteins.
                                                                                                                                                                                                     .
0
antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The proteins may be used as immunogens or antigens to obtain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagonists. The present sequence is a plant stress response protein (or fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
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                                                                                                                                                              Length 106;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                            Score 25; DB 6;
Pred. No. 1.7e+03;
                                                                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. faecium protein sequence SEQ ID 7131.
                                                                                                                                                                                                                                                                                                                                                                            ADC97504 standard; protein; 106 AA.
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                                                                                                                                                            100.0%;
50.0%; 1
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98US-0085598P.
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                                                                                                                                                                                                     4; Conservative
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71 SEFIKTDA 78
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                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                         Sequence 106 AA;
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transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomarc; tobacco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET44.
                                                                                                                                                                             Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;

 B. thuringiensis toxic crystal protein, CryET44.

                                                                   AAU02024 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                            13-SEP-2000; 2000WO-US025361.
                                                                                                                      29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                            Bacillus thuringiensis.
QEFIDSDA 67
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9
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                                                   AAU02024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that are highly expressed in uterine tumour tissue and which have anticancer and oytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling BSTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that BSTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. ANY59941-Y60328 represent protein engagements encoded by the human endometrium tummour cDNA library derived
                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dahl E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel human nucleic acid (cDNA) sequences (A)
                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                  Endometrium; human; tumour; cancer; anticancer; cytostatic; EST: treatment; uterine; gene therapy; expressed sequence tag.
                                      Length 106;
                                   Score 25; DB 7; Length 10
Pred. No. 1.7e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Human endometrium tumour EST encoded protein 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST fragments represented in AAZ41981-242121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                        AAY60038 standard; protein; 108 AA.
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50.0%; I
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                                                                 Conservative
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Best Local Similarity
4, Conserve
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75 MEFIKEDY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-591957/51.
                                                                                           1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ42013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108 AA;
           Sequence 106 AA
                                                                                                                                                                                                                                                                                                                                                                       DE19817948-A1.
                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1998;
                                                                                                                                                                                                                                               31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999.
                                                                                                                                                                                                                    AAX60038;
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                                                                                                                                                               RESULT 81
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99US-0153995P.

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0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   that are applied to plant crops to protect them from insect damage. The polymorlectides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree coll. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
                                                                                                                                                       Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                                                                                                                                                    The sequence represents a B. thuringiensis Lepidopteran-active delta-endotoxin, crystal protein CryET44. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 4; Length 109;
Pred. No. 1.8e+03;
4; Mismatches 0; Indels
   Rupar MJ;
   Gilmer AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG10474 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                        Claim 5; Page 108; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
   Donovan WP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 50.0%;
Conservative
                                                                                                                                                                                                                             insect resistance of plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:
VEFIPVDA 90
                                                                  WPI; 2001-281518/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
chu c,
                                                                                                   N-PSDB; AAS02467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG10474
ID AAG1
XX
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· 0

Gaps

0

100.0%; Score 25; DB 2; Length 108; 50.0%; Pred. No. 1.7e+03; live 4; Mismatches 0; Indels

Conservative

1 XEFIXXDX 8 ::

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9905-0139463P
9905-0139750P
9905-0139817P
9905-0140853P
9905-0140823P
9905-0140823P
9905-0140823P
9905-0140823P
9905-0140823P
9905-014292P
9905-014292P
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9905-01440175P
 18 - JUN - 1999

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20 - J
                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 8813
                                                                                                                                                                                                                                                      9905-01231800

9905-012348P

9905-012348P

9905-0128714P

9905-0128714P

9905-0128714P

9905-0128714P

9905-0128714P

9905-0130449P

9905-0130449P

9905-0130449P

9905-0131449P

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9905-0139453PP
                                                                                                                                                                                                                  2000EP-00301439
                            (first entry)
                                                                                                                                   Arabidopsis thaliana
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14-MAY-1999;
14-MAY-1999;
14-MAY-1990
                                                                                                                                                                                                                                                      05-MAR-1999,
09-MAR-1999,
23-MAR-1999,
25-MAR-1999,
01-APR-1999,
01-APR-1999,
01-APR-1999,
16-APR-1999,
119-APR-1999,
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23-APR-1999,
23-APR-1999,
30-APR-1999,
30-APR-1999,
30-APR-1999,
30-APR-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                  25-FEB-2000;
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25-MAY-1999;
27-MAY-1999;
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18-JUN-1999;
18-JUN-1999;
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14-MAY-1999;
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01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1999;
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                            17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1999
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                                                                                                                                                                                         06-SEP-2000
 AAG10474;
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hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                      990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-0125788P.
990S-012645P.
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990S-0128234P.
990S-013081D.
990S-013081P.
990S-0131449P.
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990S-013422P.
990S-013422P.
990S-013422P.
990S-013422P.
990S-0136732P.
990S-013673P.
990S-0136782P.
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99US-0139456P.
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99US-0139460P.
99US-0139461P.
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99US-0140353P.
99US-0140354P.
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                                                                                                                             2000EP-00301439
                                          Arabidopsis thaliana
                                                                                                                             25-FEB-2000;
                                                                                                                                                      25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
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10-JUN-1999;
14-JUN-1999;
                                                                      EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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08-JUN-1999
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05-MAY-1999
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                                                                                                  06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAY-1999
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  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 3; Length 11
Pred. No. 1.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 28236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG24527 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                         9905-0156596P
9905-0156596P
9905-0157117P
9905-0157865P
9905-0158029P
9905-015923P
9905-015923P
9905-015923P
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9905-015933P
9905-015963P
9905-015963P
9905-015963P
9905-015963P
9905-016076P
9905-016076P
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9905-0160980P

9905-0161404P

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9905-0161920P

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99US-0151065P.
99US-0151080P.
99US-0151303P.
99US-0151338P.
99US-0151338P.
                                                                                                              99US-0153070P.
99US-0153758P.
99US-0154039P.
99US-015473P.
99US-015513P.
99US-0155486P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
larity 50.0%;
Conservative 4
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4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 XEFIXXDX 8
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IEFICLDL
 26-AUG-1999;
27-AUG-1999;
37-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
34-SEP-1999;
34-SE
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22-0CT-1999;
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21-0CT-1999;
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21-0CT-1999;
21-0CT-1999;
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22-0CT-1999
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Best Local S:
Matches 4
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ID AAG2
XX AAG2
XX DT 17-C
XX DE Arah
XX KW Prot
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9US - 01406928 9US - 01406928 9US - 01419428 9US - 01418428 9US - 0142154P 9US - 0142290P 9US - 0142290P 9US - 0142390P 9US - 0143542P 9US - 0143642P 9US - 0144085P 9US - 0144085P 9US - 0144085P	99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-01444352P. 99US-0144884P. 99US-0145088P. 99US-0145088P. 99US-0145089P. 99US-0145089P. 99US-0145089P. 99US-0145192P. 99US-0145192P. 99US-0145192P. 99US-0145198P. 99US-0145198P. 99US-014518P. 99US-014518P. 99US-014518P. 99US-014518P. 99US-014518P. 99US-014518P.	9035 - 014 7 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
# TUN - 1999 # CUN - 1999	19-Jul - 1999; 19-Jul - 1999; 20-Jul - 1999; 20-Jul - 1999; 21-Jul - 1999; 21-Jul - 1999; 21-Jul - 1999; 22-Jul - 1999; 22-Jul - 1999; 23-Jul - 1999; 23-Jul - 1999; 23-Jul - 1999; 23-Jul - 1999; 23-Jul - 1999; 24-Jul - 1999; 25-Jul - 1999; 26-Jul - 1999; 27-Jul - 1999; 27-Jul - 1999; 27-Jul - 1999; 28-Jul - 1999;	Auge 1999 - Auge 1999
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 3; Length 110; llarity 50.0%; Pred. No. 1.8e+03; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLHR comparison related HU.IGEREC amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR57093 standard; peptide; 110 AA.
99US-0152363P.
99US-0153070P.
99US-0154039P.
99US-0154039P.
99US-0154039P.
99US-0155486P.
99US-0155486P.
99US-0155659P.
99US-0155659P.
99US-015763P.
99US-015763P.
99US-015763P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-016928P.
99US-0160361P.
99US-016077P.
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84 IEFICLDL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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 10. SEP - 1999;

10. SEP - 1999;

11. SEP - 1999;

12. SEP - 1999;

15. SEP - 1999;

22. SEP - 1999;

23. SEP - 1999;

24. SEP - 1999;

25. SEP - 1999;

26. OCT - 1999;

27. OCT - 1999;

28. SEP - 1999;

29. SEP - 1999;

21. OCT - 1999;

21. OCT - 1999;

22. OCT - 1999;

22. OCT - 1999;

22. OCT - 1999;

23. OCT - 1999;

24. OCT - 1999;

25. OCT - 1999;

26. OCT - 1999;

27. OCT - 1999;

28. OCT - 1999;

29. OCT - 1999;

29. OCT - 1999;

20. OCT - 1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG34679;
                                                                                                                                       Baum JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a polypeptide (1) containing an the memoglobulin (1g) heavy chain dimer having no 1g light chain in which the amino acid sequence of a ligand-combined partner is a receptor, a carrier protein, a hormone, a growth factor, an enzyme or a nutritive substance, but is not a subunit polypeptide encoded by a lymphocyte inducing receptor, an 1g gene super family-constituting element, a protein homologous to it, or a separated gene substitute of the variable region of at least one 1g heavy chain. Its combined partner is fused with the amino acid sequence of an 1g stationary region at its C-end and maintains its combining feature. Also described: (1) a nucleic acid maintains its combining feature. Also described: (1) a nucleic acid (1); (2) a replicable expression vector containing the nucleic acid of (1); (3) a composition containing cells transformed by the expression vector of (2); and (4) producing (1), comprising culturing the colls of (1); (3) a composition molecule and a ligand. In an example from the cell surface alignated is useful as a cell surface adhesion molecule and a ligand. In an example from the present sequence represents an amino acid sequence given in comparison with an MLHR anino acid sequence, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta endotoxin, Lepidopteran-active, crystal protein, insecticide, transgenic plant; corn, wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomato; tobaco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET45.
                                                                                                                                                                                                                                                  A fused protein consisting of a ligand-combined protein and a stable plasma protein, a polypeptide, a nucleic acid, a replicable expression vector, a composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. thuringiensis toxic crystal protein, CryET45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02025 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 11; 44pp; Japanese.
                                                                                       89US-00444625
91JP-00501520
                                             21-NOV-1990; 2002JP-00026825
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                                                                                                                                                          (GETH ) GENENTECH INC.
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GEFIWVDG 65
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Best Local Similarity
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                                                                                       22-NOV-1989;
21-NOV-1990;
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    12-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                        Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
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Pred. No. 1.8e+03;
4; Mismatches 0; Indels
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                                                                                                                                                                                                Rupar MJ;
                                                                                                                                                                                             Gilmer AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG34679 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 109; 173pp; English.
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99US-012354BP.
99US-01257BBP.
99US-0126264P.
99US-01267BSP.
99US-01264BP.
                                                                                                                                                                                             Donovan WP,
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13-SEP-2000; 2000WO-US025361.
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                                                                99US-0153995P
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                                                                                                                                                                                                                                                                                                                                                                                                                           insect resistance of plant.
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                                                                                                                                                                                                                                                             2001-281518/29.
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87 VEFIPVDA 94
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                                                                                                                                (MONS ) MONSANTO CO
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                                                                                                                                                                                                                                                             WPI; 2001-281518,
N-PSDB; AAS02468
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                                                                15-SEP-1999;
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90S - 0128714 90S - 0129845 90S - 0130407 90S - 0130407 90S - 0130810 90S - 0132484 90S - 0132484 90S - 0132484 90S - 0132486 90S - 0132486 90S - 0132486	905 - 01342189 905 - 01342189 905 - 01342189 905 - 01342189 905 - 01351248 905 - 01351248 905 - 01351248 905 - 01351248 905 - 01351248 905 - 0135128 905 - 0135128 905 - 0137528 905 - 0137528	99US-0139469P. 99US-0139461P. 99US-0139462P. 99US-0139462P. 99US-0139463P. 99US-0139763P. 99US-0139763P. 99US-0139763P. 99US-0139617P. 99US-0140354P. 99US-0140354P. 99US-014031P. 99US-0142803P. 99US-0142803P. 99US-0142803P. 99US-0142803P. 99US-0142803P. 99US-0142803P. 99US-0142803P. 99US-0143542P.
B-APR-1999 9-APR-1999 9-APR-1999 9-APR-1999 3-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999 0-APR-1999	4 WAY - 1999 WAY - 199	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 29-JUN-1999; 20-JUL-1999; 01-JUL-1999; 01-JUL-1999; 13-JUL-1999; 14-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;
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9US - 01443339 9US - 01443359 9US - 014443159 9US - 01446329 9US - 014464329 9US - 0145814P 9US - 0145086P 9US - 0145089P 9US - 0145089P 9US - 0145192P 9US - 0145192P 9US - 0145192P 9US - 0145132P 9US - 0145132P	90S - 0145913 90S - 0145913 90S - 0145919 90S - 0146386 90S - 0146389 90S - 0147302 90S - 0147302 90S - 0147302 90S - 0147302 90S - 0147303 90S - 0147303 90S - 0147303 90S - 0147303 90S - 0147303 90S - 0148319 90S - 0148319 90S - 01483419 90S - 01483419 90S - 01483419	99US-0149722P 99US-014922P 99US-0149922P 99US-0149930P 99US-0150566P 99US-015066P 99US-0151066P 99US-0151066P 99US-0151080P 99US-0151303P 99US-0151303P 99US-0151304P 99US-0151304P 99US-0151304P 99US-0151304P 99US-0151304P 99US-01558P
9-70L-199 9-70L-199 9-70L-199 9-70L-199 0-70L-199 0-70L-199 1-70L-199 1-70L-199 2-70L-199 2-70L-199 3-70L-199 3-70L-199	7. UUL-199 8. UUL-199 8. UUL-199 8. UUL-199 8. UUL-199 2. AUG-199 4. AUG-199 4. AUG-199 6. AUG-199 9. AUG-199 9. AUG-199 9. AUG-199 9. AUG-199 9. AUG-199 9. AUG-199	20. AUG-1999) 20. AUG-1999) 23. AUG-1999) 23. AUG-1999) 25. AUG-1999) 25. AUG-1999) 27. AUG-1999) 28. ESPP-1999) 29. ESPP-1999) 29. ESPP-1999) 29. ESPP-1999) 29. ESPP-1999) 29. ESPP-1999) 29. ESPP-1999) 20. CCT-1999) 20. CCT-1999) 20. CCT-1999) 21. CCT-1999) 22. CCT-1999) 23. CCT-1999) 24. CCT-1999) 25. CCT-1999) 26. CCT-1999) 27. CCT-1999)
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Gaps

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acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or blodgegadation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent opatent WO200177334 (published 18-0CT-2001) which is available in electronic format directly from WIPO at the production of 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that are applied to plant crops to protect them from insect damage. The polynucleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass; apsture grass; berry; fruit; lequme; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a B. thuringiensis Lepidopteran-active delta-
endotoxin, crystal protein CryET56. The Lepidopteran-active B.
thuringiensis delta-endotoxin polypeptides may be used as compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
                                                                                                                                                                                                                Score 25; DB 5; Length 114;
Pred. No. 1.8e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilmer AJ, Rupar MJ;
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                                                                                                                                                                                                                    100.08;
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                                                                                                                                                                                                                                     50.0%;
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                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
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                                                                                                                                                                                                                  Query Match
Best Local Similarity
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22 GEFIVCDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS02475
                                                                                                                                                                                   Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02032;
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                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
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No. 1.8e+03;
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB54747 standard; protein; 114 AA.
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                                   99US-0159330P
99US-0159637P
99US-0159637P
99US-0159584P
99US-0160741P
99US-0160764P
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99US-0161406P.
99US-0161359P.
99US-0161360P.
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99US-0160989P
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99US-0161993P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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IEFICLDL 112
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                  14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                                                                      25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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16-MAY-2002
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21-OCT-1999
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28-OCT-1999
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Matches

8

RESULT 88 ABB54747

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concluded acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene compound activity; (11) a culture comprising strains in which the gene compound the activity (12) determining the extent
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cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                      0;
                                                                                               Score 25; DB 4; Length 116; Pred. No. 1.9e+03;
                                                                                                                                    0; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #676.
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                                                                                                                  Pred. No. 1.9e
4; Mismatches
                                                                                                                                                                                                                                                                                                                 ABU15149 standard; protein; 116 AA.
                                                                                                                                      4;
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                                                                                           100.0%;
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0362699P
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                                                                                                                                      4; Conservative
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FEFIPVDA 102
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Trawick JD,
                                                                                                                                                                           1 XEFIXXDX 8
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                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
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                                                         Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200277183-A2.
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08-FEB-2002;
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Wall D,
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                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the bublished_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leinamycin biosynthesis gene cluster; Lmn; open reading frame; ORF; anti-tumour antibiotic; broad spectrum antimicrobial activity; Gram-positive; Gram-negative bacteria; chemical modification; metabolite; apo-carrier protein; holo-carrier protein; tumour; polyketide; hybrid polypeptide/polyketide metabolite; Lnm production; cytostatic.
to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of the Streptomyces atroolivaceus leinamycin (Lnm) biosynthesis gene cluster containing 71 open reading frames (ORFs -35 through -1, ORFs lnm through lnm2, and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic produced by several Streptomyces species. It exhibits broad spectrum antimicrobial activity against Gram-positive and Gram-negative bacteria, but not against fungi. The polypeptides encoded by the Lnm biosynthesis gene cluster ORFs are useful for chemically modifying a molecule in a host cell. The host cell is a bacterium or eukaryotic cell, including a
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by S. atroolivaceus leinamycin gene cluster ORF lnmV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel gene cluster responsible for synthesis of leinamycin in Streptomyces atroclivaceus useful for making various peptide and/or polyketide, and/or hybrid polypeptide/polyketide metabolites.
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                                                                                                                                                                                                                                                                                                      Length 116;
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Pred. No. 1.9e+03;
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4; Mismatches
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                                                                                                                                                                                                                                                                                                    100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces atroolivaceus.
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                                                                                                                                                                                                                                                                                                                                             Conservative
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11 PEFIFNDN 18
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                               Sequence 116 AA;
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Matches
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9905-0135629P

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9905-01317502P

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99US-0145192P.
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17-JUN-
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14-JUN-
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                                                                                                                                                                        07-JUN
       cc mammalian, yeast, plant, fungal, or insect cell. The molecule is an endogenous metabolite produced by the host cell or exogenously supplied congenous metabolite, or an amino acid, and the polypeptide is a peptide synthetase or amino transferase. The polypeptides encoded by the Lmn gene cluster converting an apo-carrier protein to a holo-carrier protein. Inm shows potent antitumour activity in tumour models in vivo. The Inm gene cluster modules and/or catalytic domains are useful for making various peptide and/or polyketide, and/or hybrid polypeptide/polyketide metabolites. The proteins encoded by the ORFs are useful alone, or in combination with other active domains to modify various target substrates. The Lmn gene cluster is useful to upregulate endogenous Lnm production to permit Lnm production in cells and/or to make various modified Lnm. Lnm, its analoque, or other polyketide, completed or hybrid polyketide/peptide metabolites are useful as the peptide or hybrid polyketide/peptide metabolites are useful as the completer completer and number of disorders, depending upon the type of metabolites. ABUI1311-ABUI1411 represent the proteins encoded by ONFS of the S. atroolivaceus leinamycin blosynthesis gene cluster
                                                                                                                                                                                                                                     o;
                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     0
                                                                                                                                                                                                              100.0%; Score 25; DB 6; Length 120; 50.0%; Pred. No. 1.9e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 32195.
                                                                                                                                                                                                                                                                                                                                AAG27381 standard; protein; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0127462P.
99US-0127462P.
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9905-0129845P.
9905-0130049P.
9905-0130891P.
9905-0131449P.
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99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0132484P
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                                                                                                                                                                                                    Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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69 NEFIQIDD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                                                                                                                           Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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21-APR-1999;
23-APR-1999;
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04-MAY-1999;
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06-MAY-1999,
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07-MAY-1999,
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us-09-660-302e-1.rag

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9908-0149476P
9908-0149472P
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9908-015066P
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99US-0157753P.
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       23 - JUL - 1999;
26 - JUL - 1999;
27 - JUL - 1999;
27 - JUL - 1999;
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28 - JUL - 1999;
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29 - AUG - 1999;
20 - AUG - 1999;
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12-AUG-1999;
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16-AUG-1999;
17-AUG-1999;
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07-SEP-1999;
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27-AUG-1999;
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15-SEP-1999;
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26-AUG-1999;
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24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated canine low affinity immunoglobulin E (IgB) receptor (CD23) polypetides and encoding nucleic acid molecules. The CD23 polypeptides can be expressed by standard recombinant methodology. The CD23 polymucleotides are useful for protecting canids from diseases mediated by CD23, for developing compounds that regulate IgB and/or CD23 lavels in a canid for treating allergy related diseases such as aropic dermatitis, asthma, hay fever and food sensitivities. The present sequence represents a CD23 receptor PsCaCD23_123
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated canine low affinity immunoglobulin B receptor nucleic ar molecule, useful for protecting canids from diseases mediated by the receptor, such as allergy, atopic dermatitis, asthma, and hay fever.
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                                                                                                                                                                             DB 3; Length 121;
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                                                                                                                                                                            k; Score 25; DB
; Pred. No. 2e+03
4; Mismatches
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           990S-0160989P
990S-0161404P
990S-0161406P
990S-0161359P
990S-0161360P
990S-0161361P
990S-0161920P
990S-0161920P
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50.0%;
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104 LEFIEEDE 111
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Best Local Similarity
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22-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
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26-OCT-1999;
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RESULT 94

AAG01456

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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                 Arabidopsis thaliana protein fragment SEQ ID NO: 42032
                                                                                                                                                                                                                                                                            990S-01267859.
990S-0127462P.
990S-0128714P.
990S-0128714P.
990S-01300407P.
990S-0130891P.
990S-0132486P.
990S-0132486P.
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990S-013444P.
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99US-0123548P.
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99US-0139750P.
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                                                                                                  Arabidopsis thaliana
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06-MAY-1999;
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11-MAY-1999;
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21-APR-19
23-APR-19
23-APR-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were brepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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4; Mismatches
                                                                                                                                                                                Human secreted protein, SEQ ID NO: 5537.
                                                                                             AAG01456 standard; protein; 124 AA.
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113 EEFIFYDY 120
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73 GEFIWMDE 80
1 XEFIXXDX 8
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Matches

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AAG34531

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99US-0140354P

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99US-014091P

99US-0141842P

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17-AUG-1999;
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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nochropic; neuroprotective; antibacterial; virucide; fundide; optidenalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder;
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Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU16559 standard; protein; 125 AA
990S-0151080P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0152363P-990S-0153758P-990S-0153758P-990S-0155659P-990S-0155659P-990S-0155659P-990S-0155629P-990S-0155629P-990S-0159232P-990S-0159233P-990S-0159233P-990S-0159638P-990S-0159638P-990S-016098P-990S-016098P-990S-016098P-990S-0161926P-990S-016098P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161926P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-990S-0161928P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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QEFIVDDL 53
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Best Local Similarity
27-AUG-1999;
30-AUG-1999;
30-AUG-1999;
01-SEP-1999;
10-SEP-1999;
11-SEP-1999;
12-SEP-1999;
22-SEP-1999;
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24-SEP-1999;
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24-SEP-1999;
06-0-CT-1999;
06-0-CT-1999;
13-0-CT-1999;
13-0-CT-1999;
13-0-CT-1999;
14-0-CT-1999;
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Matches
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cardiovascular disorder, cardiac arrest, cerebrovascular disorder, cerebral ischaemia, angiogenesis, nervous system disorder, Alzheimer, disease, infection, ocular disorder, corneal infection, wound healing, epithelial cell proliferation, skin ageing, food additive, preservative, antiproliferative.
                                                                                    2000US-0190076P
2000US-0198123P
2000US-0209451P
2000US-0214886P
2000US-0214886P
2000US-0215435P
2000US-0216480P
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2000US-02293145P
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2000US-0229513P
2000US-0239437P
2000US-0231243P
2000US-0231243P
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2000US-0232081P
2000US-0232081P
2000US-0232399P
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2000US-0232399P
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2000US-0232400P
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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2000US-0225757P.
2000US-0225758P.
                                                      2001WO-US001341
                                    WO200155322-A2
                                                                   17-JAN-2001;
                            Homo sapiens
                                             02-AUG-2001
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2000US - 0233065P.
2000US - 023423P
2000US - 023499PP
2000US - 023499PP
2000US - 0235834P
2000US - 02358336P
2000US - 02358336P
2000US - 0235836P
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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20-CC 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; -NOV-2000; -NOV-2000; -NOV-2000; 08-NOV-2000; NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 08-NOV-2000; 08-NOV-2000; NOV-2000;

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The invention relates to human novel polypeptides and their associated
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                                                                                                                 31-JAN-2000;
04-FEB-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-ANG-2000;
14-ANG-2000;
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05-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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01-SEP-2000;
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01-SEP-2000;
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21-SEP-2000;
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25-SEP-2000;
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13-OCT-2000;
                        19-SEP-2002
    egin{array} \egin{array} egin{array} \egin{array} \egin{array} \egin{array} \egin{array} \egin{array} \egin{array} \egin{array} \eg
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated nucleic acid molecules and their can concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a also used in diagnosing a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunossays e.g. radioimmunossays or enzyme linked immunosorbant assays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carbovascular disorders e.g. crachism and coular disorders e.g. corneal infections and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemetaxis. The polypeptides can also be used as a food additive or preservative to increase or derage or derage can also be used as a food additive or preservative to increase or derage and another distance or derage or derage or derage or derage or derage and increase or derage or derage and increase or derage and another distance or derage or derage or derage and another distance or derage or derage and another distance or derage or derage or derage and another distance or derage or derage and another distance or derage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; neural disorder; immune system disorder; renal disorder;
muscultar disorder; respiratory disease; reproductive disorder;
gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
hyperproliferative disorder; inflammatory disease; allergic reaction;
blood related disorder; inflammatory pressive; allergic reaction;
cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
haemostatic; antiatteriosclerotic.
                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 4; Length 125;
Pred. No. 2e+03;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                     used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 1512; 980pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU55628 standard; protein; 125 AA.
                                                                                                                                                                     Rosen CA, Barash SC, Ruben SM;
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50.0%; I
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08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0259679P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                          N-PSDB; AAS26546
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                                                                                                                                                                                                                                                                                                                 diagnosing,
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Matches
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
2000US-0225758P.
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2000US - 0234223P
2000US - 0234274P
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2000US-0236367P.
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N-PSDB; ABX73887.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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990S-0134370P
990S-0134370P
990S-0135124P
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990S-0142330E

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990S-014230E

990S-014290B

990S-014290B

990S-0142977E

990S-0143542P

990S-014408EP

990S-014408EP

990S-0144331P

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99US-0145145P
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              14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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        polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system) clubus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood appendicitis), allergic reactions and conditions (e.g. asthma) blood infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                   Score 25; DB 6; Length 125;
Pred. No. 2e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 3533.
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25 AEFIKRDD 32
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
119-APR-1999;
119-APR-1999;
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30-APR-1999;
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04-MAX-1999;
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23-APR-1999;
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PR 27-7UL-1999; 99US-0145313P.
PR 27-7UL-1999; 99US-0145313P.
PR 28-7UL-1999; 99US-0145318P.
PR 28-4UL-1999; 99US-0145318P.
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PR 24-CCT-1999; 99US-015084P.
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PR 24-CCT-1999; 99US-015
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                                                                                                100.0%; Score 25; DB 3; 50.0%; Pred. No. 2e+03; ive 4; Mismatches
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05-MAR-1999;

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12-MAY-1999;

13-MAY-1999;

14-MAY-1999;

14-MAY-1999;

15-MAY-1999;

16-MAY-1999;

21-MAY-1999;
 25-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
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PR 04-AUG-1999; 9US-0147102P.
PR 05-AUG-1999; 9US-0147102P.
PR 05-AUG-1999; 9US-0147102P.
PR 05-AUG-1999; 9US-0147102P.
PR 05-AUG-1999; 9US-0147102P.
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PR 12-AUG-1999; 9US-0147103P.
PR 12-AUG-1999; 9US-0147103P.
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PR 12-AUG-1999; 9US-014793P.
PR 12-AUG-1999; 9US-0149732P.
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PR 13-AUG-1999; 9US-0149732P.
PR 20-AUG-1999; 9US-0149732P.
PR 21-AUG-1999; 9US-0149732P.
PR 22-AUG-1999; 9US-0149772P.
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PR 22-AUG-1999; 9US-0149772P.
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PR 23-AUG-1999; 9US-0149772P.
PR 24-SEP-1999; 9US-0149772P.
PR 27-AUG-1999; 9US-0149772P.
PR 27-AUG-1999; 9US-0149772P.
PR 27-AUG-1999; 9US-0149773P.
PR 24-SEP-1999; 9US-0149772P.
PR 24-SEP-1999; 9US-0149773P.
PR 24-SEP-1999; 9US-0149773P.
PR 24-SEP-1999; 9US-015103P.
PR 24-SEP-1999; 9US-01590S.
PUS-01590S.
PUS-01590S

The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed considerably leading to the constant of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders consupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders consupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders consupplements to polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of and to produce other types of data and products dependent on DNA and amino acid sequences. Abgonolo-Abganous consumption of the sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIDO at consumption of the consument of New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder. 100.0%; Score 25; DB 3; Length 126; 50.0%; Pred. No. 2e+03; Pred. No. 2e+(4; Mismatches Claim 20; SEQ ID NO 33829; 103pp; English. Novel human diagnostic protein #3461. ABG03470 standard; protein; 126 AA. ilarity 50.0%; Pr Conservative 4; 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT; 99US-0161993P. (first entry) : | | | :: | : 46 QEFIVDDL 53 Drmanac RT, Liu C, 1 XEFIXXDX 8 WPI; 2001-639362/73 Query Match Best Local Similarity Matches 4; Conserv (HYSE-) HYSEQ INC N-PSDB; AAS67657. Sequence 126 AA; WO200175067-A2. 28-OCT-1999; 29-OCT-1999; Homo sapiens. 13-FEB-2002 11-0CT-2001 ABG03470; RESULT 100 ABG03470 PR ò g

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Search completed: September 12, 2004, 02:34:00 Job time: 111 secs

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September 12, 2004, 01:55:47; Search time 49 Seconds (without alignments) 15.705 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 300 summaries
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Sequence:

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G81321 G82310 G82310 G95987 G95987 G95987 G95987 CFYCBB G90357 G90357 H78241 H7263 G97069 A64393 H78241 H72630 G97069 A64393 H7700 A7700 A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

Description	hypothetical prote		μ	- >	hypothetical prote		L71-10 protein - f	hypothetical prote			cal		conserved hypothet	probable membrane	hypothetical prote				poly			transcription fact	replication protei	hypothetical prote		hypothetical prote	bacteriophage prot	hypothetical prote	hypothetical prote
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Oy 1 XEPIXXDX 8 RESULT 2 E45681 Physochetical 5.9K protein (gene 61.1 protein) - phage T4 C56pecides T4 C56pecides phage T4 C56pecides T4 C66pecides T4 C76pecides	25 100.0 337 1 25 100.0 337 2 25 100.0 337 2	fructose-bisphosph fructose-bisphosph indixect positive	Query Match Best Local Similarity 50.0%; Pred. No. 70; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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25 100 447 2 2011 2 2 2011 2 2 2 2 2 2 2 2 2	25 100.0 346 2	probable D-alanine	N,Alternate names: gp 61.1
25 100.0 547 2 572.23 Promoggluthin - in Public of Signature Tevision 19-Nov-1994 stoxt_Change 09-Oct-1999 572.23 Promoggluthin - in Public of Signature Tevision 19-Nov-1994 stoxt_Change 09-Oct-1999 572.23 Promoggluthin - in Public of Signature Tevision 19-Nov-1994 stoxt_Change 09-Oct-1999 572.23 572.23 Promoggluthin - in Public of Signature Tevision 54.7 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 Promoggluthin - in Public of Signature Tevision 572.23 572.23 France Tevision	25 100.0 346 2 25 100.0 347 1	probable fucose sy nonstructural prot	C.Species: phage T.4. 2.Note: host Echarichia coli
25 200 347 2 252173	25 100.0 347 2	probable oligopept	C. pate: 21-Sep-1993 #sequence revision 18-Nov-1994 #text change 08-Oct-1999
25 100.0 347 25.273 Pubmegglutinin 11 Aprilicia Aprilicia 12 Aprilicia 13 Aprilicia	25 100.0 347 2	hemagglutinin in	C.Accession: B45681; US0562
25 100.0 347 2 55276 Demogitutini 1	25 100.0 347 2	nemaggiucinin - in hemagglutinin - in	X;SellcX, H.E.; StOCHGO, C.U.; DYSOH, K.L.; ALDEILS, B.M. J. Virol, 67, 2305-2316, 1993
A	25 100.0 347 2		ween the
25 100.0 347 2 55283	25 100.0 347 2 25 100.0 347 2		A; Accession: E45681
25 100.0 347 2 55218 https://doi.org/10.00016/19.2002000000000000000000000000000000000	25 100.0 347 2		A,Status: preliminary
100 347 2 52519	25 100.0 347 2	1 1	A Molecule type: DNA
25 100.0 347 2 552195 Hemaggluttnin - in Andre: sequence extracted from NGB backbone (NCBIN.128289), NCBF:128348) 25 100.0 347 2 552198 Hemaggluttnin - in Andre: sequence extracted from NCB backbone (NCBIN.128289), NCBF:128348) 25 100.0 347 2 552198 Hemaggluttnin - in Andre: sequence extracted from NCB backbone (NCBIN.128289), NCBF:128349 25 100.0 347 2 552198 Hemaggluttnin - in Andre: sequence extracted from NCB backbone (NCBIN.128289), NCBF:128349 25 100.0 347 2 552198 Hemaggluttnin - in Andre: sequence extracted from NCB backbone (NCBIN.128289), NCBF:128349 25 100.0 347 2 552194 Hemaggluttnin - in Andre: sequence 25, DB 2, Length S4, Darchele embraches 25, DB 2, D	25 100.0 347 2		
Continue	25 100.0 347 2	1	A, Note: sequence extracted from NCBI backbone (NCBIN:128289, NCBIP:128348)
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25 100.0 347 2 859837 probable membrane probable membrane caricain [EC 3.4.2 probable membrane probable membrane caricain [EC 3.4.2 probable periphase caricain [EC 3.4.2 probable periphase at 2 881844 probable periphase caricain [EC 3.4.2 probable periphase caricain [E 3.2 probable periphase caric	25 100.0 347 2	hemagglutinin - in	A, Map Dosition: 18.973-19.135
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25 100.0 353 2 574379 Probable Arpset Proporterical proce Propor	25 100.0 350 2	oligopeptide ABC t	4; Conservative 4; Mismatches 0; Indels 0; Gaps
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25 100.0 353 2 A10670 pyrobhetical prote RESULT 3 2	25 100.0 353 2	conserved hypothet	1
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25 100.0 356 2 F37863 hypothetical prote periods sur1- PREGULT 3 25 100.0 358 2 E71866 hypothetical prote probable ABC Trans 25 100.0 359 2 H9589 hypothetical prote probable ABC Trans 25 100.0 359 2 H9582 hypothetical prote probable ABC Trans 25 100.0 361 2 F49188 protein phosphatas 25 100.0 361 2 F49188 protein phosphatas 25 100.0 362 2 S38637 hemaggluthin - in . Holroyd, S. Jagels, K. J. Leather, S.; Moule, S.; Mougall, K.; Quail, M.A.; 25 100.0 363 2 A3142 hypothetical prote Ayleference number: ABCSSION: B81922 Aylochetical prote Ayloc	25 100.0 356 2	hypothetical prote	
100.0 358 2 2 2 2 2 2 2 2 2	25 100.0 356 2	hypothetical surl-	RESOLUT 3
25 100.0 359 2 195382 100.0 259 100.0 25 100.0 25 200.0 25	25 100.0 358 2	٠.	
25 100.0 360 1 S49188 electron transfer C;Date: 0-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 25 100.0 362 2 338637 hemagglutinin - in fructose-bisphosph hemagglutinin - in fructose-bisphosph hypothetical prote hypothetical hypothetica	25 100.0 359 2	(7)	C, Species: Neisseria meningitidis
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25 100.0 363 2 A31342 fructose-bisphosph Flolroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Pollroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Particle 100.0 363 2 T20745 hypothetical prote	25 100.0 362 2	procein phospharas hemadalutinin - in	C. PACCESSENIE BALDATE BALDATE BALDATE C. PACCESSENIE BALDATE BALDATE C. P. Packhill, J. A.
25 100.0 363 2 G75050 hypochetical prote hypothetical prote A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitic A; Reference number: A81775; MUID:20222556; PMID:10761919 A; Status: preliminary A; Status	25 100.0 363 2	fructose-bisphosph	; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
25 100.0 363 2 T20745 hypothetical prote 25 100.0 364 2 E71109 hypothetical prote hypothetical prote 25 100.0 364 2 E71109 hypothetical prote 1 ALIGNMENTS	25 100.0 363 2		Nature 404, 502-506, 2000
25 100.0 364 2 E71109 hypothetical prote ALIGNMENTS	25 100.0 363 2 25 100.0 363 2		A,Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A,Reference number: A81775; MUID:20222556; PMID:10761919
ALIGNMENTS	25 100.0 364 2		A.Accession: 181922
ı	ALIGN	NMENTS	A;Factus: prelminary A;Molecule type: DNA A;Residues: 1-67 <par></par>
			A;Cross-reterences: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84063.1; PID:g737959 A;Experimental source: serogroup A, strain Z2491
			Cidenetics

Query Match 100.0%; Score 25; DB 2; Length 67; Best Local Similarity 50.0%; Pred. No. 1.3e+02; Matches 4; Conservative 4; Mismatches 0; Indels 1 XEFIXXDX 8 Q δ RESULT 1
S68260

Cybecies: Cricetulus longicaudatus (long-tailed hamster)
Cybecies: Cricetulus longicaudatus (long-tailed hamster)
Cybecies: Cricetulus longicaudatus (long-tailed hamster)
Cybecies: Os-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
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Fiftle: A novel DNA damage.ingucible transcript, gadd7, inhibits cell growth, but lacks
A,Fittle: A novel DNA damage-inducible transcript, gadd7, inhibits cell growth, but lacks
A,Accession: S68260
A,Scatus: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-38 <HOL>
A,Cross-references: EMBL:L40430

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Gaps

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RESULT 4 C96900 small conserved protein, ortholog of YAAA B. subtilis CAC0003 [imported] - Clostridium a C;Species: Clostridium acetobutylicum

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Lill protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: 562388; 562348
R;Wright, L.G.; Chen, T.; Thummel, C.S.; Guild, G.M.
J. Moll. Biol. 255, 387-40; 1996
A;Title: Molecular characterization of the 71E late puff in Drosophila melanogaster reve
A;Reference number: 562333; MUID:96152797; PMID:8568884
A;Accession: 562338
A;Accession: 562348
A;Accession: 562348
A;Accession: 56348
A;Accession: 56448
A;Accession: 56
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C;Genetics:
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50.0%; Pred. No. 2.18+02;
tive 4; Mismatches 0; Indels
                                                     Indels
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         Pred. No. 1.9e+02;
4; Mismatches 0;
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A;Crosa-references: FlyBase:FBgn0014850
A;Introns: 78,1
C;Superfamily: L71-10 protein
         50.0%;
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46 LEFINSDC
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89 LEFIGIDL
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E5 protein - human papillomavirus type 13
E5 protein - human papillomavirus type 13
E5 protein - human papillomavirus type 13
E5 protein - host Homo sapiens (man)
C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C; Accession: F42955
E; Van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G
N; Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compax
A; Reference number: A42955; MUID:92391075; PMID:1325697
A; Molecule type: DNA
A; Residues: 1-91 cVAN>
A; Residues: 1-91 cVAN>
A; Residues: Lembi:X62843; NID:960295; PIDN:CAA44652.1; PID:960301
C; Superfamily: papillomavirus E5 protein
C; Keywords: early protein
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C96900
C;Accession: C96900
C;Accession: D: Breton, G:; Omelohenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Accession: C96900
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein CAC3193 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession. G37292
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Backeriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
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A;Cross-references: GB:AE001437; PIDN:AAK77990.1; PID:g15022820; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A, Cross-references: GB:AE001437; PIDN:AAK81130.1; PID:g15026263; GSPDB:GN00168
A) Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A, Gene: CAC3193
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Pred. No. 1.6e+02;
4; Mismatches 0;
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Matches 4; Conservative
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8 TEFIKLDS 15
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24 MEFINKDD 31
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Matches 4, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CAC0003
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A, Cross-references: GB:AE004376; GB:AE003853; NID:g9657811; PIDN:AAF96329.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
C;Genetics:
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D97300
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein VCA0423 [imported] - Vibrio cholerae (strain N16961 serog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Accession: F82462

K;Heidealberg J. T.: Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035, WUID:20406833, PMID:10952301
                                                                                                                                                                                                                                             - human cytomegalovirus (strain AD169)
                                                                                                                                                                                                                                      Appothetical 13K protein (transforming region) - human cytomegalovirus (strai C;Species: human cytomegalovirus, human herpesvirus 5 C;Date: 20-Sep-1984 #text_change 17-Jul-1998 C;Date: 20-Sep-1984 #text_change 17-Jul-1998 C;Accession: A03800 R;Nelson, J.A.; Fleckenstein, B.; Jahn, G.; Galloway, D.A.; McDougall, J.K. J. Vitol. 49, 109-115, 1984 A;Title: Structure of the transforming region of human cytomegalovirus AD169. A;Reference number: A03800; MUID:84090384; PMID:6317885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C;Superfamily: human cytomegalovirus hypothetical 13K protein
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Pred. No. 2.6e+02;
4; Mismatches 0;
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Pred. No. 2.6e+02;
4; Mismatches 0;
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50.0%; F
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11 PEFIFNDN 18
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28 QEFITNDV 35
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17 AEFIALDN 24
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-119 <HEI>
                                     1 XEFIXXDX
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A, Molecule type: DNA
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T10321 R;Ahrens. C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997 A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: Z17011; MUID:97271300; PMID:9126251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A,Reference number: A86625; MUD:21235186; PMID:11337471
A,Accession: G86800
A,Status: preliminary
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59051.1; PID:g1911298
C;Superfamily: Autographa californica nuclear polyhedrosis virus EcoRI-T medium protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005176; PID:g12724395; PIDN:AAK05505.1; GSPDB:GN00146
A;Experimental source: strain II1403
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hypothetical protein Z1420 [imported] - Escherichia coli (strain O157:H7, su
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prophage pi3 protein 34 [imported] - Lactococcus lactis subsp. lactis (stra: C;Species: Lactococcus lactis subsp. lactis C;Species: Latococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: G86800
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-109 <AHR>
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Best Local Similarity 50.00
2.00 4; Conservative
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Best Local Similarity 50.0

Matches 4; Conservative
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96 LEFIKLDV 103
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GEFIVCDE 29
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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hypothetical 14.7K protein - African swine fever virus
NiAlternate names: open reading frame D129L
Cippedies: African swine fever virus, ASFV
Cipate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
Cipate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
Cipate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
Richater, R. J.; Rodriguez, J.M.; Boursnell, M.; Rodriguez, J.F.; Vinuela, E.
Gene 134, 161-174, 1993
Afritle: Two putative African swine fever virus helicases similar to yeast 'DEAH' pre-mh
A;Reference number: JT0665; MUID:94085774; PMID:8262374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pypothetical protein Imool51 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria H1093
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schludeter, T.; Simoes, N.; Tlerrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species
A;Feference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:NC_003210; PIDN:CAC98366.1; PID:g16409510; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
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A;Residues: 1-129 <YAN>
A;Cross-references: GB:U18466; NID:9780375; PIDN:AAA65332.1; PID:9780472
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A;Molecule type: DNA
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         93 VEFIVGDD 100
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120 TEFIKIDD 127
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60 IEFIKIDP 67
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Best Local Similarity
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Maxur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bundmitte to the Protein Sequence Database, April 2000
A;Reference number: 224541
A;Accession: T48833
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                                                                                      A;Cross-references: GB:AE001437; PIDN:AAK81191.1; PID:g15026331; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Genetics: A
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A;Residues: 1-123 <KUR>
A;Cross-references: GB:AE008917; PIDN:AALS2926.1; PID:g17983774; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
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C'Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001
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100.0%; Score 25; DB 2; Length 122;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-124 <SCH>
A;Cross-references: EMBL:AL353821; GSPDB:GN00112; NGSP:68B2.170
A;Experimental source: cosmid contig 68B2; strain 74
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C;Superfamily: Neurospora crassa hypothetical protein 68B2.170
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50.0%; F
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89 REFIHDDK 96
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GEFIVGDT 64
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                      A; Molecule type: DNA
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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A;Status: preliminary
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A;Residues: 1-140 <THO>

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C;Accession: A60998
R;Walters, J.A.; Dyke, K.G.H.
FEMS Microbiol. Lett. 71, 55-64, 1990
A;Title: Characterization of a small cryptic plasmid isolated from a methicillin-resists
A;Reference number: A60998
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A87354
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon
B: Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87354
A;Accession: A87354
A;Molecule type: DNA
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C;Comment: This sequence represents the only long open reading frame of a small (1613 ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AE000080; NID:g2182465; PID:g2182474; PIDN:AAB91730.1
A;Experimental source: strain NGR234
                                                                                                                                                                                          C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T28645 R;Freiberg, C.
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C;Species: Staphylococcus aureus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Dec-1999
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                                                                                                                             transcription factor homolog Y4jR - Rhizobium sp. plasmid pNGR234a C; Species: Rhizobium sp.
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Pred. No. 3.4e+02;
4; Mismatches 0;
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Pred. No. 3.5e+02;
4; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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submitted to the EMBL Data Library, November 1996
A;Reference number: Z20492
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C; Superfamily: plasmid replication protein REP
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Best Local Similarity 50.0%;
Matches 4; Conservative 4
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Best Local Similarity 50.0%;
Matches 4; Conservative 4
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47 PEFIILDM 54
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A; Residues: 1-154 < WAL>
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13 EEFINKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A60998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: y4jR
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                                                            RESULT 22
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g097212
probable acetyltransferase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 10-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
R;Nolling, J: Breton, G:; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q:; Gibson, R.; Lee, J. Daly, M.J; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Reference number: A66900; MUID:21359325; PMID:21359325
A;Accession: G97212
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D191333

Probable protein-tyrosine-phosphatase (EC 3.1.3.48) Cj1258 [imported] - Campylobacter je C;Species: Campylobacter je-juni C;Species: Campylobacter je-juni C;Date: 31.Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: D81333

R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyphycocomic pathogen Campylobacter jejuni reveals hyphycocomic pathogen pathogen pathogen Campylobacter jejuni reveals hyphycocomic pathogen pathogen pathogen Campylobacter jejuni reveals hyphycocomic pathogen pathoge
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A;Cross-references: GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CAB73512.1; PID:g696869
A;Experimental source: serotype O2, strain NCTC 11168
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A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-149 - KUR>
A,Cross-references: GB:AE001437; PIDN:AAK80490.1; PID:g15025561; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
C,Genetics:
A,Gene: CAC2539
A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64436.1; PID:g1572541 C;Genetics:
A;Gene: tnpA
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C;Superfamily: protein-tyrosine-phosphatase, low molecular weight
C;Keywords: phosphoric monoester hydrolase
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                                                                                                                                                                                          Length 140;
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                                                                                                                                                                                   ; Score 25; DB 2; Length 14
Pred. No. 3.1e+02;
4; Mismatches 0; Indels
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50.0%; P
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Best Local Similarity 50.0
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Best Local Similarity
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51 LEFIVIDV 58
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AG1755

Dacteriophage protein homolog lin2588 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Accession: AG1755
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
L; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species
A;Title: Comparative genomics of Listeria species
A;Tele: Comparative genomics of Listeria species
A;Accession: AG1755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 cGLA>
A;Residues: 1-160 cGLA>
A;Cross-references: GB:ALS92022; PIDN:CAC97815.1; PID:gl6415125; GSPDB:GN00178
A;Experimental source: strain Clip11262
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D83883
Cypothetical protein BH1868 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83883
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
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hypothetical protein VC2388 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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A,Gene: lin2588
C,Superfamily: Streptococcus phage phi-01205 hypothetical protein
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50.0%; Pred. No. 3.6e+02;
ive 4; Mismatches 0; Indels
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50.0%; Pred. No. 3.6e+02;
ive 4; Mismatches 0; Indels
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Matches 4; Conservative
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REFIAODR 33
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Matches 4; Conserv
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Cispecies: Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cipate: 14-Sep-2001
Cipate: 15-Sep-2001
Cipate: 15-Sep-2001
Cipate: 16-Sep-2001
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Dacession: 576232
C;Accession: 576232
C;Accessio
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A,Residues: 1-157 <KAN>
A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18491.1; PID:g165357
A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18491.1; PID:g165357
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Gantics:
A,Start codon: GTG
C;Superfamily: Synechocystis hypothetical protein s110272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uncharacterized conserved protein CAC0166 [imported] - Clostridium acetobutylicum
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A;Cross-references: GB:AE005673; NID:g13422099; PIDN:AAK22829.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0844
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A.Reference number: S74322; MUID:97061201; PMID:8905231
A.Accession: S76232
A.Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                              100.0%; Score 25; DB 2; Length 154;
50.0%; Pred. No. 3.5e+02;
iive 4; Mismatches 0; Indels
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Best Local Similarity 50.0°
Matches 4; Conservative
                                                                                                                                                                                                                                                                          4; Conservative
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123 VEFIENDI 130
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39 TEFINODF 46
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us-09-660-302e-1.rpr

Length 163;

Score 25; DB 2; Length 16 Pred. No. 3.7e+02; 1; Mismatches 0; Indels

100.0%;

Similarity 50.0 4; Conservative

Query Match Best Local S: Matches 4

A;Gene: BH1868

REFIRIDI 18 1 XEFIXXDX 8

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A; Cross-references: GB:AL591985; PIDN:CAC49567.1; PID:g15141054; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Cience 293, 668-672; 2001
A; Athurhors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Ielaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Keference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                             RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Accession: G95987
C;Accession: G95987
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. US.A. 98 9889-9894, 2001
A;Title: The complete sequence of the 1,683-46 pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
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A;Residues: 1-167 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52248.1; PID:g17983034; GSPDB:GN00190
A;Experimental source: strain 16M
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                                            Gaps
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             Pred. No. 3.7e+02;
1; Mismatches 0;
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Pred. No. 3.8e+02;
4; Mismatches 0;
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                                      4;
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105 DEFIIKDF 112
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SEFIVADN 64
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A;Molecule type: DNA
A;Residues: 1-170 <KUR>
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A;Experimental source: strain C-125
C;Genetics:
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A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73419.1; PID:g696859
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
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                                    and
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Nucleic Acids Res. 28, 4317-4331, 2000
A/Tile: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Status: preliminary
A/MACession: D83883
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Length 164;

100.0%; Score 25; DB 2; Length 16 50.0%; Pred. No. 3.7e+02; cive 4; Mismatches 0; Indels

Conservative

Best_Local Similarity Matches 4; Conserv

Query Match

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Db

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A;Gene: Cj1165c C;Superfamily: primosomal operon 14K protein

A;Accession: G81321 A;Status: preliminary A;Molecule type: DNA

DB 2; Length 165;

100.0%; Score 25;

C;Superfamily: peptide methionine sulfoxide reductase

A; Genetic code: SGC3

Query Match

A; Gene: msrA; UU289

A; Experimental source: serovar 3; biovar 1

A;Residues: 1-165 <GLA>
A;Cross-references: GB:AE002125;

A;Status: preliminary A;Molecule type: DNA

A; Reference number: A82870

A; Accession: G82910

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A;Status: preliminary
A;Status: Dreliminary
A;Molecule trype: DNA
A;Molecule trype: DNA
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07650.1; GSPDB:GN0
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07650.1; GSPDB:GN0
C;Genetics:
A;Genetics:
A;Genetics:
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Cispecies: Wibrio cholerae
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cipates 10: 18-Aug-2006
RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
Andradson, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Affitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MuID:20406833; PMID:10952301
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A, Molecule type: DNA
A, Recession: B94024
A, Molecule type: DNA
A, Resperimental source: strain PR-6
A, Experimental source: strain PR-6
A, File: Cloning and sequencing of the genes encoding the alpha and beta subunits of C-A, Reference number: A94017, MUID: 85063716; PMID: 6438628
A, Reference number: A94017, MUID: 85063716; PMID: 6438628
A, Rote: Agmentallum quadruplicatum
A, Residues: 1-172 < PIL-
A, Cross-references: GB: K02659; NID: 9142176; PIDN: AAB05341.1; PID: 9142177
A, Experimental source: strain PR-6
C, Superfamily: phycocyanin
C, Keywords: chromoprotein; methylated amino acid; photosynthesis; phycocyanobilin C; Keywords: chromoprotein; methylated amino acid; photosynthesis; phycocyanobilin (Cys) (covalent) #status predicted
F, 82/Binding site: phycocyanobilin (Cys) (covalent) #status predicted
F, 153/Binding site: phycocyanobilin (Cys) (covalent) #status predicted
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C;Species: Synechococcus sp.
C;Species: Synechococcus sp.
C;Species: 13-Aug-1986 #text_change 11-Jun-1999
C;Accession: B94017; A00321; A22972
R;de Lorimier, R.; Bryant, D.A.; Porter, R.D.; Liu, W.Y.; Jay, E.; Stevens JProc. Natl. Acad. Sci. U.S.A. Bl., 7946-7950, 1994
A;Title: Genes of the alpha and beta subunits of phycocyanin.
A;Reference number: A94024; MUID: 85088525; PMID: 6096868
A;Note: Agmenellum quadruplicatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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50.0%; Pred. No. 3.9e+02;
ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                      Score 25; DB 2;
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4; Mismatches 0;
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137 NEFIVMDS 144
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GEFISSDK 23
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                                                                                                                                                                                                              Uncharacterized conserved protein CAC1676 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Accession: G97106 [B. M.V. ] Breton, G. ] Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
J. Saccession: G97106
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97106
A;Accession: G97106
A;Accession: G97106
A;Residues: 1-170 «KUR>
A;Residues: 1-170 «KUR>
A;Residues: 1-170 «KUR>
A;Coss-references: GB:AE001437; PIDN:AAK79642.1; PID:g15024638; GSPDB:GN00168
C;Genetics: C;Genetics: Clostridium acetobutylicum ATCC824
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Chlamydia trachomatis Liacucumcals (serotype D, strain UM3/CX)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71530
B;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Accession: E71530
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A;Cross-references: GB:AE001303; GB:AE001273; NID:g3328718; PIDN:AAC67896.1; PID:g332871
A;Experimental source: serotype D, strain UM-3/Cx
C;Genetics:
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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50.0%; P
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136 SEFIVVDR 143
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5 REFIGADV 12
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50 LEFIDNDY
      XEFIXXDX
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Cispecies: Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cidacession: H97205
Rivolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
T.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Accession: A64300; MUID:96337999; PMID:8688087
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C;Genetics:
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A;Cross-references: GB:AE001437; PIDN:AAK80435.1; PID:g15025501; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C.Accession: A64393
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr_2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                        probable kinase from adenilate kinase family, FLAR-like protein [imported]
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Pred. No. 4.1e+02;
4; Mismatches 0; Indels
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C;Superfamily: hypothetical protein MJ0745
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EEFIKMDK 65
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23 SEFIITDD 30
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                                  A;Cross-references: GB:AE004329; GB:AE003852; NID:g9657211; PIDN:AAF95770.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Clostridium acetobutylicum (Cipateria) - Clostridium acetobutylicum (Cipateria) - Clostridium acetobutylicum (Cipateria) - 197084

Rivolling, U.; Breton, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Balty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4822-4838, 2001

A; Reference number: A96900; MUD:21359325; PMID:21359325

A; Reference number: A96900; MUD:21359325; PMID:21359325

A; Status: preliminary

A; Moleçule type: DNA
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G10944 dehydrorhamnose 3,5 epimerase (rfbC-2) [imported] - Sulfolobus solfataricus d10P-4-dehydrorhamnose 3,5 epimerase (rfbC-2) [imported] - Sulfolobus solfataricus G; psecies: Sulfolobus solfataricus C; psecies: Sulfolobus solfataricus C; pate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C; Accession: G90357
G; Accession: G90357
G; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jaffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Reference number: A99139
A; Ressidues: 1-176 < KUR>
A; Residues: 1-176 < KUR>
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A;Residues: 1-176 -KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79463.1; PID:g15024442; GSPDB:GN00168
A;EXPERIMENTAL SOURCE: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC1495
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C;Superfamily: shikimate kinase; shikimate kinase homology
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C;Superfamily: dTDP-4-dehydrorhamnose 3,5-epimerase
                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 2;
50.0%; Pred. No. 4e+02;
cive 4; Mismatches
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50.0%; Pred. No. 4e+02;
iive 4; Mismatches
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Matches 4; Conservative
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KEFIISDK 162
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30 MEFIDSDT 37
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Best Local Similarity
Matches 4; Conserva
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A; Residues: 1-174 <HEI>
                                                                                                                C;Genetics:
A;Gene: VC2629
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Divisory photosystem I chain III - Odontella sinensis chloroplast
NiAlternate names: photosystem I plastocyanin-binding chain
CiSpecies: chloroplast Odontella sinensis
CiDate: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
CiAccession: 578329
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinens
A;Reference number: 57823
A;Accession: 57832
A;Accession: S7832
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DN
A;Residues: 1-185 <KCW>
A;Residues: 1-185 <KCW>
A;Cross-references: EMBL:Z67753; NID:g1185127; PIDN:CAA91702.1; PID:g1185219
A;Cose-references: EMBL:Z67753; NID:g1185127; DIDN:CAA91702.1; PID:g1185219
C;Genetics:
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Hypothetical protein MTH578 - Methanobacterium thermoautotrophicum (strain Delta H)

Gispecies: Methanobacterium thermoautotrophicum (strain Methanobacterium thermoautotrophicum Delta H: func Michaeler (strain 179, 7135-7155, 1997

A) Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func A; Reference number: A69000; MUID:98037514; PMID:9371463

A) Accession: E69176

A) Astatus: preliminary; nucleic acid sequence not shown; translation not shown

A; Residues: 1-186 < MTH>
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A;Experimental source: strain Delta H
C;Genetics:
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 18-Aug-2003
C;Accession: G97069
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: chloroplast
C;Superfamily: photosystem I chain III
C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I
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50.0%; Pred. No. 4.3e+02;
ive 4; Mismatches 0; Indels
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Best Local Similarity 50.03
Matches 4; Conservative
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122 DEFIIQDE 129
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71 VEFISGDV 78
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Matches 4; Conserv
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C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72630
C;Accession: H72630
C;Accession: H72630
A;Accession: H72630
BNA Res. G, 83-101, 1999
BNA Res. G, 83-101, 1999
BNA Res. G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72630
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83913
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05826.1; GSPDB:GN00
A;Experimental source: strain C-125
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A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80502.1; PID:d1044288; PID:g510
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Accession: C83913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 2; Length 181; 50.0%; Pred. No. 4.2e+02; cive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <BEV>
A;Cross-references: EMBL:AL162508
A;Experimental source: cultivar Columbia; BAC clone T7H20
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 2;
50.0%; Pred. No. 4.2e+02;
iive 4; Mismatches 0;
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C, Genetics:
A, Gene: APE1503
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Best Local Similarity 50.0%
...... 4; Conservative
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Best Local Similarity 50.0 Matches 4; Conservative
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100 IEFINNDF 107
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121 MEFIYHDS 128
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Best Local Similarity
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          A;Accession: T48241
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A;Introns: 158/1
A;Note: T7H20.250
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A;Gene: BH2107 C; Genetics

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RESULT 45

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C; Superfamily: precorrin-6Y methylase CbiT

A; Gene: CAC1378

C; Genetics:

Conservative

Query Match
Best Local Similarity
4; Conserve

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RESULT 49

1 XEFIXXDX 8

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A; Molecule type: DNA
A; Residues: 1-192 <br/>
A; Residues: 1-192 <br/>
A; Residues: 1-192 <br/>
A; Residues: 1-192 <br/>
A; Cross-references: GB: Moszer, I. Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte: G.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature: 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle. C.C., I. Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogawara, A.; Ogawara, A.; Codega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, P.; Schroeter, P.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, J.; A; Wirtle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Archesian, Racesian, Rac
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A;Experimental source: strain 168
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: AD3014
R; Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Stwood, D. W.; Setubal, J.C.; Cant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: B47700; D69634
B; Beljer, L; Milson, R.P.; Holmberg, C.; Rutberg, L.
J. Gen. Microbiol. 139, 349-359, 1993
A; Title: The glpp and glpF genes of the glycerol regulon in Bacillus subtilis.
A; Accession: B47700; MUID:93171878; PMID:8436953
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                        Gaps
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C;Keywords: transcription antitermination; transcription regulation
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                                    50.0%; Pred. No. 4.4e+02; ive 4; Mismatches 0;
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Similarity 50.0%; H
4; Conservative 4;
                                                                                        4; Conservative
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177 KEFILLDL 184
                                                                                                                                                                                           1 XEFIXXDX 8
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Matches 4; Conserv
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Matches
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A70100
hypochetical protein BB0001 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Decies: Borrelia BB0001
C;Decies: Borrelia BB0001 - Lyme disease spirochete)
C;Decies: A70100
C;Decies: A
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97069
A;Gratus: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <KUR>
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A;Experimental source: strain B31
C;Superfamily: Borrelia burgdorferi hypothetical protein BB0001
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A;Experimental source: Clostridium acetobutylicum ATCC824
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C;Genetics:
A;Gene: RC0043
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A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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50.0%; Pred. No. 4.38+02;
ive 4; Mismatches 0; Indels
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C; Superfamily: hypothetical protein H10304

Conservative

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Local Similarity

Query Match

:|||::|: 156 KEFIFADN 163

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A;Residues: 1-190 <KLE>

Query Match

A; Accession: A70100

1 XEFIXXDX 8

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probable regulator [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995 C;Species: Escherichia coli (c;Date: 18-Jul-2001 C;Date: 18-Jul-2001 C;Date: 18-Jul-2001 E;Date: 2001 E;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable regulator ykgK [imported] - Escherichia coli (strain 0157:H7, substrain EDL933 C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R. Percession: walstar III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001

Nature 409, 529-533, 2001

A. Aritile: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A. Accession: G85519

A. Accession: G85510

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C;Species: Bscherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: F64755
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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50.0%; Pred. No. 4.5e+02;
iive 4; Mismatches 0; Indels
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Pred. No. 4.5e+02;
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Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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93 GEFIEGDK 100
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72 TEFINRDN 79
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72 TEFINRDN 79
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1 XEFIXXDX 8
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R;Agostoni Carbone, M.L.; Panzeri, L.; Melchioretto, P.; Carignani, G.; Feroli, F.; Fron
submitted to the Protein Sequence Database, May 1996
A;Reference number: 864577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g40440 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84829
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; Wnite, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Mature 402, 761-768, 1999
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A;Residues: 1-196 <AGO>
A;Cross-references: EMBL:273036; NID:g1323455; PID:e243683; PID:g1323456; GSPDB:GN00007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: E84829
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-194 <STO>
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                                                    A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-192 <KUR>
A;Cross_references: GB:AE008689; PIDN:AAL44530.1; PID:g17742143; GSPDB:GN00187
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N;Alternate names: hypothetical protein G9140
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
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Pred. No. 4.5e+02;
4; Mismatches 0; Indels
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Pred. No. 4.4e+02;
4; Mismatches 0;
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50.0%; F
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A;Map position: linear chromosome
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A;Map position: 7R
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Best Local Similarity 50....
A; Conservative
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159 DEFIVGDD 166
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             A; Accession: AD3014
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RESULT 58

1 XEFIXXDX 8

A;Gene: ykgK

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Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUD:21537279; PMID:11679669
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH1169 #11169
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                  hypothetical colled-coil protein [imported] - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                               C, Accession: T50322
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, submitted to the EMBL Data Library, January 2000
A;Reference number: Z25061
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-202 AMD>
A;Residues: 1-202 AMD>
A;Residues: 1-202 AMD>
A;Residues: SAMBL:AL136536; PIDN:CAB66453.1; GSPDB:GN00067; SPDB:SPBC1703.09
A;Experimental source: strain 972h(-); cosmid c1703
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A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein lin0754 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB1527
                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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Pred. No. 4.7e+02;
1; Mismatches 0; Indels
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Pred. No. 4.7e+02;
4; Mismatches 0; Indels
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50.0%; E
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                                        51
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TEFIPADV 45
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-202 <GLA>
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Franslation initiation factor IF-3 - Mycoplasma pneumoniae (strain ATCC 29342)

NyAlternate names: hypothetical protein C09_orf201

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

A;Variety: ATCC 29342

C;Date: 25-Feb-1997

R;Hibert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Ree. 24, 4420-4449, 1996

A;Ritle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g1673684; PIDN:AAB95687.1; PID:g167368 to the EMBL Data Library, November 1996
                                                                                                                                             A;Cross-references: GB:AE000136; GB:U00096; NID:g2367103; PIDN:AAC73397.1; PID:g2367106;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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                        A; Accession: F64755
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-196 < BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: T027AP
R;Lorbiecke, R.; Sauter, M.
Submitted to the EMBL Data Library, February 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AF050200; NID:g2952337; PID:g2952338
C;Genetics:
A;Gene: SIP2
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 25; DB 2; Best Local Similarity 50.0%; Pred. No. 4.5e+02; Matches 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z14738
A;Accession: T02787
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Note: the nucleotide sequence was submitted
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable submergence induced protein 2 - rice
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Query Match
Best Local Similarity 50.0
Matches 4; Conservative

1-199 <LOR>

A; Residues:

:|||::|: 34 KEFIPVDK 41

Db ð

RESULT 59

1 XEFIXXDX 8

4; Conservative

1 XEFIXXDX 8

Query Match Best Local Similarity Matches 4; Conserva

A;Gene: infC A;Genetic code: SGC3

0;

Gaps

0

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probable ribosomal protein L25 PA4671 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (strain PAO1) C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Dec-2002 C;Accession: G83060 C;Accession: G8306 C;Accession: G8306 C;Accession: Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Vuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim Nature 406, 959-964, 2000 A;Aritle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Accession: G83060 A;Accession: G83060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <STO>
A;Cross-references: GB:AE004882; GB:AE004091; NID:g9950939; PIDN:AAG08058.1; GSPDB:GN00
A;Experimental source: strain PAO1
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   A; Cross-references: GB: U67494; GB: L77117; NID: 91591120; PIDN: AAB98415.1; PID: 91591133;
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C;Species: Scytalidium lignicolum
C;Species: Scytalidium lignicolum
C;Species: Scytalidium lignicolum
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 31-Dec-1993
C;Accession: A28864
R;Maita, T.; Nagata, S.; Matsuda, G.; Maruta, S.; Oda, K.; Murao, S.; Tsuru, D.
D: Blochem. 95, 465-475, 1984
A;Title: Complete amino acid sequence of Scytalidium lignicolum acid protease B.
A;Reference number: A28864; MUID:84185536; PMID:6370989
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50.0%; Pred. No. 4.8e+02;
ive 4; Mismatches 0; Indels
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llarity 50.0%; Pred. No. 4.8e+02;
Conservative 4; Mismatches 0
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A;Residues: 1-204 <MAI>
C;Keywords: aspartic proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: PA4671
C;Superfamily: 508 ribosomal protein L25
                                                                           A; Map position: REV386963-386349
C; Superfamily: dCTP deaminase
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                 4; Conservative
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130 AEFIIEDF 137
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144 PEFIEVDM 151
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38 DEFIIYDD 45
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Best Local Similarity
Matches 4; Conserv
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G83060
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C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Accession: AC1595
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mao, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;fitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Accession: F64353
Rsquence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: F64353
Rsbult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstook, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A;Atle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUD:96337999; PMID:8688087
A,Accession: F64353
A,Accession: F64353
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A,Residues: 1-204 <BUL>
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1169
                                                                                                                                                                                                                                                  A;Status: preliminary
A;Status: Dreliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:NC_003210; PIDN:CAC98838.1; PID:g16410149; GSPDB:GN00177
A;Cross-references: GB:NC_003210; PIDN:CAC98838.1; PID:g16410149; GSPDB:GN00177
A;Experimental source: strain EGD-e
A;Genetics:
A;Genetics:
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A;Residues: 1-203 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96531.1; PID:g16413773; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1300
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Pred. No. 4.7e+02;
4; Mismatches 0; Indels
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50.08; P
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Best Local Similarity 50.v*
...a 4; Conservative
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Best Local Similarity 50.03
Matches 4; Conservative
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57 NEFIVRDQ
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C;Species: Sinorhizobium meliloti
Chate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 02-Aug-2002
C;Accession: F95892
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna:
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
Pritle: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end.
A;Reference number: A95842; MUID:21396508; PMID:11481431
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Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 15-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain 1021, megaplasmoid, properties of the following strain 1021, megaplasmoid psymb Symb Scaliber, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F., Soience, 293, 668-672, 2001
A; Atuthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K.A; Reference number: Ag6039; MUID:21368234; PMID:11474104
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R, Simpson, A.J.G.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Athuthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
                                                                                                                                                                                                                                                                                                                                                                                                                       (strain
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                                                                                                                                                                                                                                                                                                                                                                                                   probable glutathione S-transferase protein (imported) - Sinorhizobium meliloti
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
                                                                                                                                 Gaps
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4.8e+02;
ches 0;
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Pred. No. 4.8e+
4; Mismatches
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C;Superfamily: hypothetical protein b0838
                                                          100.0%;
50.0%; I
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Conservative
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25 VEFIRDDI 32
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-208 <SIM>
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A;Residues: 1-208 <KUR>
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Date: 22-Oct-2010 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: C98270
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 244, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Recession: C98270
A;Recession: C98270
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-205 cKUR>
A;Ccoss-references: GB:AE007870; PIDN:AAK89685.1; PID:g15159591; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L_2230
A;Map position: linear chromosome
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A;Experimental source: strain Madrid E
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Cidate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
Cidate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
Cidatesion: H1671
Richardson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A.Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A.Reference number: A71630; MUID:99039499; PMID:9823893
A.Reference number: A71630; MUID:99039499; PMID:9823893
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
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50S ribosomal protein 14 [imported] - Rickettsia conorii (strain Malish 7)
50S ribosomal Bactes: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: E97825
R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Soience 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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50.0%; Pred. No. 4.8e+02;
iive 4; Mismatches 0;
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A;Gene: rplD; RP658
C;Superfamily: Bscherichia coli ribosomal protein L4
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A,Gene: rplD
C,Superfamily: Escherichia coli ribosomal protein L4
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ribosomal protein 14 - Rickettsia prowazekii
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172 DEFIVGDD 179
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A;Status: preliminary
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C;Genetics:
A;Gene: RC1320
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C;Date: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-209 <KUR>
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C;Species: Dacersion: 140484; A69729; S49364
R;Martinussen, J;Glaser, P; Andersen, P.S.; Saxild, H.H.
J;Bacteriol. 177; 271-274, 1995
A;Title: Two genes encoding uracil phosphoribosyltransferase are present in Bacillus sub A;Reference number: 140473; MUID:95095982; PMID:7798145
A;Accession: 140464
A;Reference number: Informaty; translated from GB/EMBL/DDBJ
A;Rocassion: 140464
A;Reference sembl:238002; NID:9556877; PIDN:CAA86111.1; PID:9556887
A;Rocassion: 1209 < RES>
A;Residues: 1-209 < RES>
A;Crossreferences: EMBL:238002; NID:9556877; PIDN:CAA86111.1; PID:9556887
A;Crossreferences: EMBL:238002; NID:956877; PIDN:CAA86111.1; PID:9556887
A;Crossreferences: EMBL:238002; NID:956877; PIDN:CAA86111.1; PID:9556887
A;Rosidues: 1-209 < RES>
A;Crossreferences: EMBL:238002; NID:956877; PIDN:CAA86111.1; PID:9556887
A;Rosidues: D:9 RESS>
A;Crossreferences: EMBL:238002; NID:956877; PIDN:CAA86111.1; PID:9556887
A;Rosidues: D:9 RESS>
A;Crossreferences: EMBL:238002; NID:956897; PIDN:CAA86111.1; PID:9556887
A;Rolecule type: DA
A;Rolecule type: DA
A;Rolecule type: DA
A;Rolecule type: D: Fritz, C.; Futita, M.; Fujita, Y.; Fuma S.; Galizzi, A.; Galler
C; Branch S; Brundler, S.; Rumanc, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Korieger, M.; Ruychors: Louber, J.; Lazarevic, V.; Lee, S.H.; Parro, V.; Pohl, T.M.; Parro, V.; Pohl, T.M.; Rager, M.; Riyolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, A.; Serollon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serollon, A; Authors: Schleich, S.; Schroeter, R.; Sechfone, F.; Sekiguchi, J.; Sesonlon, A; Authors: Schleich, S.; Schroeter, R.; Sesonlon, S.; Schroeter, R.; Sesonlon, S.; Schroeter, R.; Sechelon, S.; Schroeter, R.; Sechelon, S.; Schroeter, R.; Sechelon, S.; Schroeter, R.; Sechelon, S.; Schroeter, R.; Sechelo
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvain M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A;Genetics: annotation C;Genetics: A;Genetics: A;Genet
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Accession: T17329
A;Accession: T17329
A;Accession: T17329
A;Accession: T17329
A;Accession: Database, September 1999
A;Accession: T17329
A;Accession: T17329
A;Accession: Database
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A;Experimental source: fetal brain; clone DKFZp564K2364
C;Genetics:
A;Note: DKFZp564K2364.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein DKFZp564K2364.1 - human (fragment)
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Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 2; ilarity 50.0%; Pred. No. 4.9e+02; Conservative 4; Mismatches 0;
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159 VEFIRHDR 166
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144 PEFIEVDL 151
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.; Danchin, A.
A., Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A., Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A., Reference number: A69580; MUID:98044033; PMID:9384377
A., Accession: A69729
A., Status: nucleic acid sequence not shown; translation not shown
A., Residues: 10.09 < KUN>
A., Residues: 10.09 < KUN & KUN 
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Dates: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: C71647
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9923893
A;Reference number: A71630; MUID:99039499; PMID:992893
A;Reference number: A71630; MuiD:99039499; PMID:993893
A;Reference number: A71630; MuiD:99039499; PMID:993893
A;Reference number: A71630; MuiD:99039499; PMID:993893
A;Reference number: A71630; MuiD:99039499; PMID:993861237; PIDN:CAA15275.1; PID:938613
A;References: GB:A7235273; GB:A7235269; NID:93861237; PIDN:CAA15275.1; PID:9386123A; GGene: RP851
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50.0%; Pred. No. 4.9e+02;
tive 4; Mismatches 0; Indels
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125 REFIVVDP 132
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69 IEFIDADY 76
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Length 209;

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Mismatches

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A; Accession: S28955
A; Molecule type: mRNA
A; Residues: 1-210 cABBA
A; Cross-references: EMBL:X65868; NID:g4973; PIDN:CAA46698.1; PID:g4974
C; Superfamily: dTMP kinase
C; Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
F; 14-21/Region: nucleotide-binding motif A (P-loop)
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
R;Abaigar, L.T.; Yeh, Y.I.S.; Jong, A.Y.
Biochim. Biophys. Acta 1132, 222-224, 1992
A;Title: Functional and structural conservation of Schizosaccharomyces pombe dTMP kinas:
A;Reference number: S28955; MUID:93003330; PMID:1327149
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CiDate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
CiAccession: A85098
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colo Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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A,Molecule type: DNA
A,Residues: 1-211 <STO>
A,Residues: GB:NC_001268; NID:g7267654; PIDN:CAB78082.1; GSPDB:GN00140
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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... No. 4.9e+02;
0; Indels
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Pred. No. 4.9e+02;
4; Mismatches 0;
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Pred. No. 4.9e+02;
4; Mismatches 0;
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50.0%; I
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175 LEFITLDA 182
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Best Local Similarity
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A; Map position: 2
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                                                                                                                                                                                                                                    protein ROBES.1 [imported] - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C.Accession: E89009
R.anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Reference number: A75000; MUID: 990650613; pmID: 9851916
A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A.Rote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Status: preliminary
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:chr_V; PIDN: AAB52275.1; PID:g1938440; GSPDB:GN00023; CESP:R08E5.
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Saccession: T41553
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
Submitted to the EMBL Data Library, June 1998
A;Reference number: Z22001
A;Reference number: Z22001
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-210 < WOOD>
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dTMP kinase (EC 2.7.4.9) - fission yeast (Schizosaccharomyces pombe)
c:Species: Schizosaccharomyces pombe
C:Species: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jan-2001
C:Accession: S28955
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Pred. No. 4.9e+02;
4; Mismatches 0; Indels
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100.08;

1-209 <STO>

A; Residues:

50.0%;

Conservative

Best Local Similarity Matches 4; Conserv

A; Map position: 5 A; Gene: R08E5.1

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1 XEFIXXDX 8

Score 25; DB 2; L Pred. No. 4.9e+02; 4; Mismatches 0;

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100.0%; 50.0%; P

Query Match Post Local Similarity 50.0

:|||::|: LEFITLDA 183

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RESULT 78

1 XEFIXXDX 8

A;Introns: 45/1; 110/3 C;Superfamily: dTMP kinase

A;Gene: SPDB:SPCC70.07c A;Map position: 3

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C,Species: Borrelia burgdorferi (Lyme disease spirochete)
C,Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Dec-2002
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Pred. No. 5e+02;
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50.0%;
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Best Local Similarity 50.03
Matches 4; Conservative
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172 PEFIELDL 179
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Best Local Similarity
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                                                                                                   Cispecies: Pseudomonas aeruginosa
Cispecies: Pseudomonas aeruginosa
Cispecies: Pseudomonas aeruginosa
Cispecies: Pseudomonas aeruginosa
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Ciaccession: A83521
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Reference number: A835521
A;Accession: A83521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-212 <STO>
A,Cross-references: GB:AE004532; GB:AE004091; NID:g9946896; PIDN:AAG04379.1; GSPDB:GN001
A,Experimental source: strain PA01
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E82675
hypothetical protein XF1489 [imported] - Xylella fastidiosa (strain 9a5c)
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C;Keywords: aspartic proteinase; hydrolase
F;1-5/Domain: signal sequence (fragment) #status predicted <SIG>
F;6-211/Product: scytalidopepsin B #status predicted <MAT>
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50.0%; Pred. No. 5e+02;
ive 4; Mismatches 0; Indels
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136 AEFIIEDF 143
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Best Local Similarity
                    XEFIXXDX
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A;Molecule type: DNA
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R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: A69505

A;Actual: preliminary: nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: D91019
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:AE000962; GB:AE000782; NID:g2689285; PIDN:AAB89213.1; PID:g264849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:AE006641; NID:g13813505; PIDN:AAK40691.1; GSPDB:GN00155
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C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2003
C;Accession: A69505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SSO0361 [imported] - Sulfolobus solfataricus
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                                                                                                                                                                          Score 25; cc.
Pred. No. 5.1e+02;
Pred. No. 5.1e+02;
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             A; Experimental source: cultivar Columbia
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50.0%; E
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177 NEFIFSDS 184
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124 AEFIKADV 131
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85 REFIEGDE 92
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                                        C,Genetics:
A,Gene: TINY
A,Map position: 5
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T01076
R;Huang, E.N.; de la Bastide, M.; Habermann, K.; Schutz, K.; Shekher, M.; Vil, M.D.; Presubmitted to the EMBL Data Library, August 1998
A;Description: BAC F18A17 from chromosome V, containing TINY at 60.5 cM.
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 22-Oct-1999
C;Accession: E69339
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69339
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: GB:AE001055; GB:AE000782; NID:g2689378; PIDN:AAB90523.1; PID:g264989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutathione transferase (EC 2.5.1.18) homolog GST1 - potato
N;Alernate names: glutathione S-transferase; pathogenesis-related protein prpl-1
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
R;Strittmatter, G.
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A;Accession: T07595
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-217 <STR>
A;Cross-references: EMBL:J03679; NID:g862344; PIDN:AAA68430.1; PID:g169549
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A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-218 <HUA>
A;Cross-references: EMBL:AC005405; NID:g3406034; PID:g3406035
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40 AEFIRADV 47
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29 YEFIEEDL 36
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A,Introns: 103/3
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hypotherical protein lmo2166 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
R;Gaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Atitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1345
A;Atatus: preliminary
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N;Alternate names: orfl protein
N;Alternate names: orfl protein
N;Alternate names: orfl protein
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: A29891; A34765; Ā44221; H72851
J; Nirol. 62, 463-471, 1988
A;Title: Functional mapping of Autographa californica nuclear polyhedrosis virus genes A;Reference number: A93041; MJD:88091055; PMID:2826808
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A;Mclecule type: DNA
A;Mclecule type: DNA
A;Mclecule type: DNA
A;Mclecule type: DNA
A;Mclecule type: LNA
A;Mcsilly, D.R.; Passarelli, A.L.; Goldman, I.F.; Miller, L.K.
B;O'Reilly, D.R.; Passarelli, A.L.; Goldman, I.F.; Miller, L.K.
A;Cross-references: ENBL:M18857; N990
A;Title: Characterization of the DA26 gene in a hypervariable region of the Autographa
A;Reference number: A34765; MUID:90264832; PMID:2189022
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A;Residues: 1-225 <OAR>
A;Residues: GB:M22619; GB:M33904; NID:g332422; FIDN:AAA69846.1; FID:g896308
A;Cross-references: GB:M22619; GB:M33904; NID:g332422; FIDN:AAA69846.1; FID:g896308
R;Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D. Virology 191, 1003-1008, 1992
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A,Experimental source: strain EGD-e
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A;Molecule type: DNA
A;Residues: 1-222 cHAY>
A;Cross-references: GB:BA000007; PIDN:BAB35697.1; PID:g13361740; GSPDB:GN00154
A;Cross-references: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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Pred. No. 5.2e+02;
4; Mismatches 0;
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50.08; F
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171 KEFILPDE 178
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54 VEFIGODG 61
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Best Local Similarity
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A; Residues: 1-223 <GLA>
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                                          C,Accession: B90913
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Acession: B90913
A;Accession: B90913
A;Status: preliminary
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R,Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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A,Molecule type: DNA
A,Residues: 1-221 - KUR>
A,Cross-references: GB:AE001437; PIDN:AAK78963.1; PID:g15023894; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methyltransferase-related protein VC0113 [imported] - Vibrio cholerae (strai
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Pred. No. 5.2e+02;
4; Mismatches 0; Indels
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A;Cross-references: GB:AE004102; GB:AE003852; NID:g9654512; A;Experimental source: serogroup Ol; strain N16961; biotype: C;Genetics: A;Gene: VCO113
A;Map position: 1
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208 LEFIGNDV 215
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
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Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, U. Science 294, 849-852, 2001
Aphathors: Krefer, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makhatle. Comparative genomics of Listeria species.

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
        ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1477
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C; Sate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D90657
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mazutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shibb, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_003210; PIDN:CAD00855.1; PID:g16409692; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
                                                                                                                                                                                                             A;Cross.references: GB:AL592022; PIDN:CAC95586.1; PID:g16412782; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein lmo0328 [imported] - Listeria monocytogenes (strain EGD-e)
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A;Residues: 1-226 «KUR»
A;Cross-references: GB:BA000018; PID:g13702481; PIDN:BAB43622.1; GSPDB:GN00149
A;Experimental source: strain N315
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SA2319 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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                                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 2;
Pred. No. 5.3e+02;
4; Mismatches 0;
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4; Mismatches
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
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IEFIGEDT 113
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106 IEFIGEDT 113
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                                                                                                                      A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-226 <GLA>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-226 <GLA>
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Matches 4; Conserv
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AB1477
hypothetical protein lin0353 [imported] - Listeria innocua (strain Clip11262)
G.Species: Listeria innocua
C.Species: Disteria innocua
C.Species: J. Nov-2001
C.Species: J. Baquero, F.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
S.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                     A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Cross-references: 1-25 < cRRA
A,Cross-references: GB:S52569
R,Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
A) Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A,Reference number: A72850; MUID:94303173; PMID:8030224
A,Accession: H72851
A,Accession: H72851
A,Accession: H72851
A,Accession: H72851
A,Accession: Transinary
A,Molecule type: DNA
A,Residues: 1-225 < carry
A,Molecule type: DNA
A,Cross-references: GB:L22888; NID:9510708; PIDN:AAA66646.1; PID:9559085
C,Comment: The gene is located in a 3-kilobase Xbal genome fragment.
C,Comment: This protein is required for viral late gene expression.
genomic organization of the EcoRI-A fragment of Autographa californid
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C;Superfamily: Autographa californica nuclear polyhedrosis virus DA26 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-226 <WIL>
A;Coss-references: EMBL:Z70211; PIDN:CAA94158.1; GSPDB:GN00028; CESP:K11E4.2
A;Experimental source: clone K11E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 Accession: T23611
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                                                        A; Reference number: A44221; MUID:93079853; PMID:1333113
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50.0%; Pred. No. 5.3e+02;
tive 4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 25; DB 1;
Pred. No. 5.3e+02;
4; Mismatches 0;
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A.Reference number: 219770
A.Accession: T23611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 95
T23611
hypothetical protein K11E4.2 - Caenc C, Species: Caenorhabditis elegans C, Date: 15-Oct-1999 #sequence_revis: C, Accession: T23611
R, Gajadsty, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 30/3; 81/3; 137/3; 175/2
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50.0%;
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195 FEFINPDE 202
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GEFIIRDS 177
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Matches 4: Conserv
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A;Gene: CESP:K11E4.2
                                                                                A; Accession: A44221
A; Title: Sequence,
                                VP8 of rotavirus.
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C;Species: Pyrococcus abysis:
C;Species: Pyrococcus abysis:
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: C75210
C;Accession: C75210
A;Pescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struch; A;Accession: C75210
A;Accession: C75210
A;Accession: C75210
A;Accession: Drainnary
A;Molecule type: DNA
A;Residues: 1-27 < kAM>A;Residues: 1-28 < kAM>A;Coss-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49130.1; PID:g545763
A;Genetics:
A;Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PH0226 - Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: C71246
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yammamoto, S.; Sekin M.; Ohluku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yammazaki, J.; Kushida, N.; Oguchi DNA, Res. 7-6, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A1000; MUID:98344137; PMID:9679194
A;Accession: C71246
A;Accession: C71246
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A;Accession: C71246
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A)Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29298.1; PID:g3256615
A)Experimental source: strain OT3
A)Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sterol biosynthesis methyltransferase related PAB2213 - Pyrococcus abyssi (strain Orsay)
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A;Gene: PH0256
C;Superfamily: conserved hypothetical protein MJ1123; bioC homology
F;39-144/Domain: bioC homology <BIOC>
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100.0%; Score 25; DB 2; Length 227;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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GHR_SHEEP
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COOS_METKA
GHR_HUMAN
NPRE_BACCE
MANC_PIRSP
YL53_YEAST
MANB_PIRSP
SYP_BUCAP
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
YOIK BPT4

TO YOUR BPT4

AC P39228; Q9TOV8;

DT 01-FEB-1995 (Rel. 31, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

BE Hypothetical 5.9 kDa protein in Gp58-sp intergenic region.

GN YOIK OR 61.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T4-like viruses.
NCBI_TaxID=10665;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE=22514363; PubMed=12626685;
Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
"Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
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MEDLINE=92391075; PubMed=1325697;
Van Ranst M., Fuse A., Fiten P., Beuken B., Pfister H., Burk R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: comparison of the genome organizations."; Virology 190:587-596(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 AA; 10245 MW; FCB0CE86BB7E5DE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                      26 26 I -> T (IN REF. 1).
54 AA; 5897 MW; 972C516A70FE8609 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 50;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB ilarity 50.0%; Pred. No. 90; Conservative 4; Mismatches
                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR008736; Papilloma E5A. Pfam; PF05776; Papilloma E5A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                       EMBL; AF158101; AAD4250811; -. PPR; E45681; E45681. F45691. Hypothetical protein. CONFLICT 26 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X62843; CAA44652.1; -. PIR; F42955; W5WL13.
                                                                                                                                                                                                                                                                        EMBL; S57514; AAB25712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||::|:
KEFIKEDM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probable E5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Opdenakker G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Early protein SEQUENCE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VES HPV13
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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VES_HPV13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Tears;
MEDLINE=9816332; PubMed=9504814;
Molloy M.P., Bolis S., Herbert B.R., Ou K., Tyler M.I., van Dyk D.D.,
Willox M.D., Gooley A.A., Williams K.L., Morris C.A., Walsh B.J.;
"Establishment of the human reflex tear two-dimensional polyacrylamide
gel electrophoresis reference map: new proteins of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Lipophilin, a novel heterodimeric protein of human tears.";
FEBS Lett. 432:163-167(1998)
-!- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
-:- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
-:- STRAMUGYINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
-!- STBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
[MAMMAGLOBIN B) MONOMER ASSOCIATED HEAD TO HEAD.
-!- TISSUE SPECIFICITY: Expressed in thymus, trachea, kidney, steroid responsive tissues (prostate, testis, uterus, breast and ovary)
                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mammaglobin B precursor (Mammaglobin 2) (Lipophilin C) (Lacryglobin)
SCGREtoglobin family 2A member 1).
SCGB2A1 OR MGB2 OR UGB3 OR LIPHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and salivary gland.
MASS SPECTROMETRY: MW-8854.94; METHOD=Electrospray; RANGE=19-95.
SIMILARITY: Belongs to the uteroglobin family. Lipophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98385871; PubMed=9720917;
Lebrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
Glasgow B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of mammaglobin B, a novel member of the uteroglobin
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99026127; PubMed=9806831;
Becker R.M., Darrow C., Zimonjic D.B., Popescu N.C., Watson M.A.
Fleming T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99167354; PubMed=10066439; Zhao C., Mguyen T., Vatsifov T., Glasgow B.J., Lehrer R.I.; "Lipophilins: human peptides homologous to rat prostatein."; Biochem. Biophys. Res. Commun. 256:147-155(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 19-46 AND 60-78, AND MASS SPECTROMETRY
                                                                                                                                                                95 AA
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lectrophoresis 18:2811-2815(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF071219; AAC79996.1; -. EMBL; AJ224173; CAA11865.1; -.
                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene family.";
Genomics 54:70-78(1998).
                                                                                                                                                              STANDARD;
ω
                        : | | | :: |:
1 MEFIPUDV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 19-85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic value.",
1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=rears;
                                                                                                                                                                MGBB HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                            .) (POTENTIAL).
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O
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MEDINE=91045079; PubMed=2235495;
TAYLOR M.T.M., Brunt A.A., Coutts R.H.A.;
"Conservation of the 3' terminal nucleotide sequence in five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION.
-!- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 101;
                                                                                                                                                                                                                                                                                                                                          DB 1; Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 18:6127-6127(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
11.6 kDa protein (Putative nucleic acid-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C4-TYPE (POTENTIAL).
SBDF36C3A14A5091 CRC64;
                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (1
0719738289F89F8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; 50.0%; Pred. No. 1e+02; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AA
                                                                                                                                               ProDom; PD029354; Mamgb/prostatn; 1.
PROSITE; PS00403; UTEROGLOBIN 1; FALSE NEG.
PROSITE; PS00404; UTEROGLOBIN 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                              Pred. No. 94;
4; Mismatches
                                                                                                                                                                                                                                                         MAMMAGLOBIN B
                                                                                                                                                                                                                                                                                                                                          Score 25;
                                         GO; GO:0005497; F:androgen binding; NAS
                                                           InterPro; IPR003627; Mamgb/prostatn.
InterPro; IPR000329; Uteroglobin subf.
InterPro; IPR006038; Uteroglobin_supf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S12170; S12170.
InterPro; IPR002568; Carla C4.
Pfam, PF01623; Carla C4; 1.
Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AA; 11626 MW;
                                                                                                                           Pfam; PF01099; Uteroglobin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carnation latent virus (CLV).
                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                              95 AA; 10884 MW;
                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X55897; CAA39386.1; -.
HGNC:7051; SCGB2A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                     18
95
68
                                                                                                                                                                                                                 Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
4, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
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QEFIDSDA 54
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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89 LEFIGIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=12164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carlaviruses.
                        MIM; 604398;
                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNBP_CLV
ID _VNBP_CLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                Best
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12950922;
Zhang Y.-C., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Zhang Y.-C., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";
Mol. Microbiol. 49:1577-1593(2003).
-!- FUNCTION: Involved in the transcription termination process (By
                                                                                                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
N utilization substance protein B homolog (NusB protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 12:
50.0%; Pred. No. 1.3e+02;
50.0%; Pred. No. 1.3e+02;
                                                           l protein.
118 AA; 13412 MW; 3FEBF7A48658E208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription termination, Complete proteome. SEQUENCE 129 AA; 15150 MW; 161923DD8535AlCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                   100.0%; Score 25; DB 1; 50.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STW2_MOUSE STANDARD; PRT; 146 AA. P813091.
28-159-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Stromal interaction molecule 2 (Fragment).
STIMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the nusB family.
                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
EMBL; K01263; -; NOT_ANNOTATED_CDS.
PIR; A03800; QQBE8H.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016748; AA004804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, MF 00073; -; 1.
InterPro; IPR006027; NusB.
Pfam; PF01029; NusB; 1.
                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                            :|||::|:
28 OEFITNDV 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 IEFIKDDH 37
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                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                          1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUSB OR SE1205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUSB_STAEP
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUSB_STAEP
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                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
   S K BR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                         Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 1; Length 109; Pred. No. 1.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA; 12053 MW; 597E7F7137389454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 04) Last annotation update)
Hypothetical (Rel. 40, Last annotation update)
Hypothetical 13 kba protein in transforming region.
Human cytomegalovirus (strain AD169)
                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ECORI-T site protein ETM homolog.
                                                                                                                109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     Nucleopolyhedrovirus.
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96 LEFIKLDV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early protein.
                                                                                                             VETM NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y13K HCMVA
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                                                                                                                                         010307;
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Y13K HGWVA
IN 13K HGWVA
DT 21-JUJ.
DT 21-JUJ.
DT 16-OCT.
DE HYPOCHA
OC VIRUSE
OC NCELT.
RN NEDLIN
RX MEDLIN
RX MEDLIN
RX MEDLIN
RY NELON
R
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PARTY SECONDARY
o;

Gaps

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"Molecular basis of symbiosis between Rhizobium and legumes.";
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InterPro; IPR002569; PMSR.
Pfam; PF01625; PMSR; 1.
                                                                                                                                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicute
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                         :|||::|:
47 PEFIILDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSRA OR UU289
                                                                                                                                                                                                                                                                                                                                                                                              MSRA UREPA
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation-
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                                                                                                                                                         proteins.;
Biochem. J. 357:673-688 (2001)

-!- FUNCTION: Possible adhesion molecule with a role in early hematopoiesis by mediating attachment to stromal cells. Influences the survival and/or proliferation of B cell precursors. Binding to cells requires Mm(II) (By similarity)

-!- SUBGNAT: Oligomer with STIM1 (By similarity)

-!- SUBCELIULAR LOCATION: Type I membrane protein. Cell surface
                                                                       STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
MEDLINE=1355314; PubMed=11463338;
Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S.,
Van Stekelenburg L., Eid J.-P., Senior P.V., Kazenwadel J.S.,
Shandala T., Sanit R., Smith P.J., Dziadek M.A.;
"Identification and characterization of the STIM (stromal interaction molecule) gene family: coding for a novel class of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                          (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 1; Length 14:50.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSTON SAM DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 AA; 17321 MW; 503740533EEB0F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA
                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2151156; Stim2.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR001660; SAM.
SMART; SW00454; SAM; 1.
PROSITE; PS50105; SAM DOWAIN; 1.
Cell adhesion; Transmëmbrane; Coiled co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical 17.3 kDa protein Y4JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAM.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF328907; AAK82339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pNGR234a.
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  musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 XEFIXXDX 8
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                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
55
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P55518;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 151; 50.0%; Pred. No. 1.6e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methorine sulfoxide reductase msrA (EC 1.8.4.6)
methionine-S-oxide reductase) (Peptide Met(O) reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 151 AA; 17262 MW; F8B42BCF7845E03F CRC64;
                                !- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 AA
                                                                                                                                                                                                                                                                                                                                     EMBL, AE000080; AAB91730.1; -.
PIR, T28645.
InterPro; IPR001789; Response_reg.
SMAR; SMO448; REC; 1.
PROSITE; PS50110; RESPONSE REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002125; AAF30698.1; -. HSSP; P54149; 1FVG.
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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"Gamma-N-methylasparagine in phycobiliproteins. Occurrence, location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 236:167-170(1988).
                                                                                                                                                                                                                                                                                                        MEDLINE-85063716; PubMed-6438628;
Filot TJ., Fox J.L.;
"Cloning and sequencing of the genes encoding the alpha and beta
subunits of C-phycocyanin from the cyanobacterium Agmenellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duerring M., Huber R., Bode W., "The structure of gamma-N-methylasparagine in C-phycocyanin from Mastigocladus laminosus and Agmenellum quadruplicatum.",
                                                                                          Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                        de Lorimier R., Bryant D.A., Porter R.D., Liu W.-Y., Jay E., Stevens S.B. Jr., "Genes for the alpha and beta subunits of phycocyanin."; Proc. Natl. Acad. Sci. U.S.A. 81:7946-7950(1984).
                                                                                                                                                                                                                                                                                                                                                                         quadruplicatum.";
Proc. Natl. Acad. Sci. U.S.A. 81:6983-6987(1984).
           23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERTIARY STRUCTURE AROUND METHYLATED SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 262:17350-17355(1987).
                                                                                                                                                                                         MEDLINE=85088525; PubMed=6096868;
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88087010; PubMed=2447072;
                                                          C-phycocyanin beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klotz A.V., Glazer A.N.;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=32049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and biosynthesis
                                                                                                                                                                             STRAIN=PR-6;
                                                                                                                                                                                                                                                                                                                                                                                                                       METHYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delinible 2136508; PubMed=11481431; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., Enter P.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., Enter Sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.", Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

-! CATALYIC ACTIVITY: (-)-ureidoglycolate + H(2)O = glyoxylate + 2 NH(3) + CO(2).

-! PATHWAY: Degradation of allantoin (purine catabolism); third step.
-! SIMILARITY: Belongs to the ureidoglycolate hydrolase family.
                                                                                                                                          Gaps
                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Froteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium. NCBI_TaxID=382;
                                                                                                        Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 1; Length 170; 50.0%; Pred. No. 1.8e+02; ive 4; Mismatches 0; Indels
                                                                                                   100.0%; Score 25; DB 1; Length 16
50.0%; Pred. No. 1.7e+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00616; -; 1.
InterPro; IPR00747; Ureidogly_hydro.
InterPro; IPR00747; Ureidogly_hydro.
Hydrolase; Purine metabolism; Plasmid; Complete proteome.
SEQUENCE 170 AA; 18930 MW; 051CACE71CEF9CDF CRC64;
                                                                      678DC470BBE22AAD CRC64;
                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
ALLAI OR RELI67 OR SMB20873.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                     170 AA
ProDom; PD003489; PMSR; 1.
TIGRFAMs; TIGR00401; msrA; 1.
Oxidoreductase; Complete proteome.
ACT_SITE 11 BY SIMILARITY.
SEQUENCE 165 AA; 19341 MW; 678DC470BBE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL603646; CAC49567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pSymB (megaplasmid 2)
                                                                                                                  Local Similarity 50.0
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                       : | | | :: |:
105 DEFIIKDF 112
                                                                                                                                                                   1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G95987; G95987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1021;
                                                                                                                                                                                                                                                                                  RHIME
                                                                                                     Query Match
                                                                                                                                                                                                                                                                               ALL1 RHIN
Q92UG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                  RESULT 11
ALL1 RHIME
                                                                                                                                 Matches
      STARBA
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                                                                                                                                                                                                                                                                                                                                                                HSSP, P07119; ICPC.
InterPro; IPR001659; Phycobilisome.
InterPro; IPR006247; Phycocyanin_b.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
TIGRFAMS; TIGR01339; phycocy_beta; 1.
Phycobilisome; Blectron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
from the phycobiliprotein complex.
-!- SUBUNIT: Heterodimer of an alpha and a beta chain.
-!- PTM: Contains two covalently linked bilin chromophores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHYCOCYANOBILIN CHROMOPHORE, PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70D82718A77767EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Le
50.0%; Pred. No. 1.8e+02;
.ive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 72 MET
82 82 PH3
153 153 PH3
172 AA; 18336 MW; '
                                                                                                                                                                                                                                                                                                              EMBL; K02660; AAB05343.1; -.
EMBL; K02659; AAB05341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GEFISSDK 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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Gaps

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4; Conservative

Matches

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1 XEFIXXDX 8

172 AA.

PRT;

STANDARD;

OPKNVI;

RESULT 13 AROK_VIBCH

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                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. Rep. 13:336-342(1995).
-!- FUNCTION: Probably participates in efficiency of electron transfer from plastocyanin to P700 (or cytochrome c553 in algae and cyanobacteria). This plastocyanin-docking protein contributes to the specific association of plastocyanin to PSI.
-!- SUBCELLUIAR LOCATION: Associated with lumenal side of the
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-22514363; PubMed-12626685;
Miller E.S., Kutter E., Mosig G., Arisaka.F., Kunisawa T., Ruger W.;
                                                                                                                             Mzhavia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S. Maya M., Bidermiller J., Canada D., Traoy J., Galbreath K., Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M.; "The 10.7 kb 'nonessential' region of bacteriophage T4 between the
                                                                                                                                                                                                                   genes tk and nrdC: twenty new t4 genes, generally conserved among T-even phages."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, stramenopiles, Bacillariophyta, Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
              no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freis
"The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 1; Lengu...-4 No. 1.9e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMPL, ALLES I protein.

Hypothetical protein.

RROUENCE 175 AA; 20757 MW; 12ABE25E9AEC5219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FFB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Photosystem I reaction centre subunit III (PSI-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the psaF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 AA
                                                                                                                                                                                                                                                                                                                                                                                          "Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.9e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Odontella sinensis (Marine centric diatom)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF158101; AAD42639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
50.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U76612; AAB26974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 50.v-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                Viruses; dsDNA viruses,
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thylakoid membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 IEFIKKDI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 XEFIXXDX 8
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                                                                                                         SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ODOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P49483;
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PSAF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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0
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20406833; PubMed=10925301;
Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Bisen J.A., Nelson W.C., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406,477-483(2000).
-!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01128; SHIKIMATE KINASE; 1.
Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 20.7 kDa protein in nrdC-mobD intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 174; 50.0%; Pred. No. 1.8e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the shikimate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IP (BY SIMILARITY).
206FABCBFA9981CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fifth step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence
10-OCT-2003 (Rel. 42, Last annotatic
Shikimate kinase (RC 2.7.1.71) (SK).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype Ol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP, MF 00109; -; 1.
InterPro, IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004329; AAF95770.1; -. HSSP; P10880; 1SHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01100; SHIKIMTKNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                        STANDARD;
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30 MEFIDSDT 37
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                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
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                                                                     AROK VIBCH
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Query Match

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YOSD BPT4

SEPTIFE

RESULT 14 YOSD_BPT4

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  CONFLICT
CONFLICT
CONFLICT
CONFLICT
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                                                       SEQUENCE
                                                                                                                                                                                                                         GLPP_BA(
P30300;
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Matches
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     SFFF
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          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
Fraser C.M., Casjens S., Hanng W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                  Gaps
     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Telomeres of the linear chromosomes of Lyme disease spirochaetes: nucleotide sequence and possible exchange with linear plasmid
                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                    InterPro; IPR003666; PSI PsaF.
Pfam; PF02507; PSI PsaF; 1.
Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
SEQUENCE 185 AA; 20747 MW; 16C70038FAD4F048 CRC64;
                                                                                                                                                                                  .
0
                                                                                                                                                      DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casjens S., Murphy M., Delange M., Sampson L., van Vugt R.,
     as its content
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> M (IN REF. 2)
                                                                                                                                                                     2e+02;
                                                                                                                                                                                                                                                                                            Y001_BORBU STANDARD; PRT; 190 AA. 051035; 051894; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                  Pred. No. 2e+0
4; Mismatches
institutions as long
                                                                                                                                                      100.0%; Score 25; 50.0%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sh-2-82;
MEDLINE=98065594; PubMed=9402027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol, 26:581-596(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001115; AAC66406.1; -. EMBL; AF008218; AAB93996.1; -.
                                                             EMBL; Z67753; CAA91702.1; -. PIR; S78329; S78329.
                                                                                                                                      Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein BB0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:580-586(1997).
                                                                                                                                                                                                                       :[||::|:
166 QEFISNDL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A70100; A70100.
TIGR; BB0001; -.
                                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             telomeres.";
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Y001_BORBU
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brigarell S.C., Bron S.,

RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Deviner K.M., Dusterhoff A., Ehrlich S.D., Emmerson D.T.,

RA Ghim S.Y., Claser P., Officeu A., Gollightly E.J., Grandi G.,

RA Ghims C.Y., Claser P., Goffeau A., Gollightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koninosstein G., Krogh S., Kumano M.,

RA Kobayashi Y., Koetter P., Koninosstein G., Krogh S., Kumano M.,

RA Kobayashi Y., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Dazarevic V.,

RA Medina N., Wellado R.P., Mizuno M., Woestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

Ra Rieger M., Rivolta C., Roch B., Roche B., Rose M., Sadaie Y.,

RA Scanlam E., Schleich S., Schroeter R., Scoffene F.,

Sekiguchi J., Sekowska A., Seros S.J., Serror P., Shin B.S., Soldo B.,

RA Sorokin A., Tamakoshi A., Tarakani H., Takamaru K.,

RA Presecani E., Pujic P., Purnelle B., Rababahi H., Takamaru K.,

RA Sorokin A., Tarakai T., Terpstra P., Tognoni A.,
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the glyB marker, many genes encoding transporter proteins, and the ubiquitons hir neem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beijer L., Nilsson R.-P., Holmberg C., Rutberg L.; "The glpp and glpF genes of the glycerol regulon in Bacillus subtilis.";
                                                                                                                                                                          Score 25; DB 1; Length 190; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
cake operon antiterminator regulatory protein.
                                                                                                                                                                                                                                         Indels
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                                                                                                                    FBFCE799CD827B45 CRC64;
                         KI -> NL (IN REF. 2).
S -> P (IN REF. 2).
S -> I (IN REF. 2).
                                                                                                                                                                                                                                         ..
   EDL -> GDI (IN REF.
                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Microbiol. 139:349-359(1993).
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MEDLINE=93171878; PubMed=8436953;
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                                                                                                                    22491 MW;
                                                                                                                                                                             100.08;
                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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41
81
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177 KEFILLDL 184
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                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                    190 AA;
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                                                                                                                                                                                                                                                                                                     1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLPP OR BSU09270
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34
40
53
81
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YKGK ECOLI
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                                                                                                                                                                                        P53317;
                                                                                                                                              RESULT 19
YGSC YEAST
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ECOLI
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                     Nature 390:249-256(1997).
-!- FUNCTION: IN THE PRESENCE OF GLYCEROL 3-PHOSPHATE, THIS PROTEIN IS THOUGHT TO ENHANCE PRANSCRIPTION.
-!- SIMILARITY: TO E.COLI YGCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                        EMBL; M99611; AAA22489.1; -.
EMBL; Y14079; CAA74427.1; -.
EMBL; A14079; CAA74427.1; -.
EMBL; A29108; CAB12755.1; -.
EMBL; A2700; B47700.
Subtilist; BG10185; glpp.
InterPro; IPR006699; FMN enzyme.
InterPro; IPR006699; G3P anitierm.
Pfam; PF04309; G3P anitierm.
If Glycerol metabolism; Transcription regulation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- SIMILARITY: None obvious.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid sym_pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 192; 50.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000070; AAB92444.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 192 AA; 20638 MW; A2B0B75IAD579EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         21609 MW; E3B9A85C5AFA3949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 20.6 kDa protein Y4DX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.1e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::|:
71 AEFICQDI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                             192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y4DX RHISN
P55423;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
Y4DX_RHISN
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                                                        0;
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of a 17.9 kb region from Saccharomyces cerevisiae chromosome VII reveals the presence of eight open reading frames, including BRF1 (TFIIIB70) and GCNS genes."; Yeast 13:373-377(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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0
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Feroli F., Carignani G., Pavanello A., Guerreiro P., Azevedo I
Rodrigues-Pousada C., Melchioretto P., Panzeri L.,
Agostoni Carbone M.L.;
                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last amoutation update)
Hypothetical 22.3 kDa protein in MGA1-GCN4 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 196;
100.0%; Score 25; DB 1; Length 192; 50.0%; Pred. No. 2.1e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
Hypothetical protein ykgK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AA
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                  PRT;
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                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                        STANDARD;
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GermOnline, 141563; -.
SGD, S0003483; YGR251W.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||::|:
93 GEFIEGDK 100
                                                                                                                                                                   118 VEFIEDDP 125
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                                                                                                                1 XEFIXXDX 8
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     Query Match
Best Local Similarity
Matches 4; Conserv
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us-09-660-302e-1.rsp

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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bifunctional deaminases/diphosphatase (MjDCD-DUT) (DCD/DUT) [Includes: Deoxycytidine triphosphate deaminase (RC 3.5.4.13) (dCTP deaminase); Deoxyuridine 5'-triphosphate nucleotidohydrolase (RC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96317999; PubMed=8688087;

Bult C.J. White O., Olsen G.J. Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li H., Xu H., Graham D.E., White R.H.,
"The Methanococcus jannaschii dCTP deaminase is a bifunctional
deaminase and diphosphatase.",
"5. Biol. Chem. 278:11100-11106 (2003).
-!- FUNCTION: Catalyzes two consecutive reactions to form dUMP using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION, MASS SPECTROMETRY, AND MUTAGENESIS OF ASP-135 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initiation factor; Protein biosynthesis; Complete proteome.
SEQUENCE 201 AA; 23145 MW; 3E14B9FA797C80C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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Pred. No. 2.2e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA
               SIMILARITY: Belongs to the IF-3 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22538493; PubMed=12538648;
                                                                                                                                                                                                                                                                                                         EMBL, AE000004; AAG34732.1; -. PIR; S73365; S73365. HASP, P03000; ITTF. HAMP: MF 00080; -1. InterPro; IPP001288; IF3. Pfam; PF00707; IF3_C; I. Pfam; PF00707; IF3_C; I. ProDom; PD002880; IF3; I. TIGRFAMS; TIGR0168; InfC; I. PROSITE; PS00198; IF3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (dUTPase) (dUTP pyrophosphatase)]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
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44 NEFILIDE
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Matches
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DCD_METJA
               SO WE WE WE WE WAS A SECOND COLOR CO
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Nucleic Acids Res. 24:4420-4449(1996),

Nucleic Acids Res. 18-3 binds to the 30S ribosomal subunit and shifts the equilibrum between 70S ribosomes and their 50S and 30S subunits in favor of the free subunits, thus enhancing the availability of 30S subunits on which protein synthesis initiation begins.

-!- SUBUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                           Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                               STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Rrley M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                               Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K. Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Li Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodom; PD000307; HTH LuxR; 1.
SWART; SM00421; HTH LUXR; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 196 AA; 23274 MW; 5A3676E17E9793B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-NoV-1997 (Rel. 34, Last annotation update)
Translation initiation factor IF-3.
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MEDLINE=97105885; PubMed=8948633;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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MEDLINE=99039499; PubMed=9823893;
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Best Local Similarity 50.v.
4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                      134 PEFIEVDV 141
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25 VEFIRDDI 32
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P39149;
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-!- SIMILARITY: Belongs to the L25P family of ribosomal proteins.
-!- CATALYTIC ACTIVITY: dCTP + H(2)O = dUTP + NH(3).
-!- CATALYTIC ACTIVITY: dUTP + H(2)O = dUMP + diphosphate.
-!- COFACTOR: Magnesium.
-!- ENZYME REGULATION: Inhibited by dTTP.
-!- PATHWAY: De novo synthesis of thymidylate.
-!- SABUNIT: Homohexamer (Probable).
-!- MASS SPECTROMETRY: MW=23619; MW ERR=94; METHOD=MALDI.
-!- MASC SPECTROMETRY: MW=24619; MG ERR=94; METHOD=MALDI.
-!- MISCELLANEOUS: Optimal DH is 7.5. Retained over 70% of its activity when heated at 90 degrees Celsius for 10 min.
-!- SIMILARITY: Belongs to the dCTP deaminase family.
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"A ribosomal protein from Thermus thermophilus is homologous general shock protein.";
Biochimie 78:915-919(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 204; 50.0%; Pred. No. 2.2e+02; ative 4; Mismatches 0; Indels
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Thermus thermophilus.
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MEDLINE=97295226; PubMed=9150868;
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30-MAY-2000 (Rel. 39, Last sequ
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67494; AAB98415.1; -. PIR; F64353; F64353.
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38 DEFIIYDD 45
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Best Local Similarity
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P56930;
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-!- FUNCTION: This protein binds directly and specifically to 23S rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the L4P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 207;
                                                                                                                                                                                                                  Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 20
50.0%; Pred. No. 2.2e+02;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Threat PF005733; Ribosomal L4; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEOUENCE 207 AA; 23288 MW; AA652123EB22797E CRC64;
                                                                                                                                                            E6C214CAF141316C CRC64;
                                                                                                                                                                                                                  ; Score 25; DB 1;
Pred. No. 2.2e+02;
4; Mismatches 0;
EMBL; X94435; CAA64209.1; -.
PDB; 1FEU; 25-UUN-01.
InterPro; IPR001021; Ribosomal L25.
TIGRRAMS; TIGR00731; ctc TL5; ī.
TIGRRAMS; TIGROFT, FRNA-binding; 3D-structure.
SEQUENCE 206 AA; 23218 MW; E6C214CAF141316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 39, Last sequence update)
50S ribosomal protein L4.
RPLD OR RP658.
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                                                                                                                                                                                                                         100.0%; Score 25;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Ra Derriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Bronillet S., Burschi C.V. Caldwell B., Capuano V., Carter N.M.,
RA Broinilet S., Burschi C.V. Caldwell B., Capuano V., Carter N.M.,
RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
Guiseppi G., Guy B.J., Hagap K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Joris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,
RA Joris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J. J., Lazarevic V.,
RA Medina N., Mellado R.P., Mazuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mazuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sato T., Scanlan E., Schlerch E., Roche B., Roche B., Rose M., Sadaie Y.,
Schiduchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Schiduch A., Tacconi E., Takanshi H., Takematu A.,
Schiduch A., Wambutt R., Wedler H., Wanner E., Vassarotti A.,
Vlari A., Wambutt R., Wedler E., Wedler H., Wanneroeger T.,
William A., Wambutt R., Wedler H., Yannen E., Yasumoto K., Yata K.,
R. Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
Ribrilis H., R. R. Weller H., Wanner E., Pacherium Bacillus
R. Takeuchi M., Tananer E., Porbikawa H., Danchin A.,
R. Takeuchi M., Tananer E., Porbikawa H., Panchin A.,
R. Takeuchi M., R. Wanner E., Verbikawa H., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                       (UMP pyrophosphorylase)
                                                                                                                                                                                                                                                                              Martinussen J., Glaser P., Andersen P.S., Saxild H.H.;
"Two genes encoding uracil phosphoribosyltransferase are present in
Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: UMP + diphosphate = uracil + 5-phospho-
alpha-D-ribose 1-diphosphate.
COFACTOR: Magnesium (By similarity).
                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
01-FEB-1995 (Rel. 31, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Uracil phosphoribosyltransferase (EC 2.4.2.9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Pyrimidine salvage pathway.
-!- SIMILARITY: Belongs to the UPRTase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG10345; upp.
HAMAP; MF 01218; -; 1.
InterPro; IPR000836; PRTransferase.
InterPro; IPR005765; Ura_phspho_trans.
                                                                                                                                                                                                                                                        MEDLINE=95095982; PubMed=7798145;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 177:271-274(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z38002; CAA86111.1; -. EMBL; Z99122; CAB15706.1; -.
                                                                                              UPP OR IPC-35D OR BSU36890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; I40484; I40484.
HSSP; Q26998: 1RD3
                                                                                                                 Bacillus subtilis.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=1423;
                                                                                                                                                                                                                                     STRAIN=168
                                                                     (UPRTase)
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A Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles U., Baker S., Basham D., Bowman S., A Brooks W., Even D., Baker S., Basham D., Bowman S., Rajandream M.A., Davis P., Elabell T., Fraser A., Brown B., Conin A., Davis P., Feltwell T., Fraser A., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Radlorods S., Goble A., Hamin N., Harris D., Hiddlgo J., Hodgeon G., R. Holroyd S., Hornsby T., Howarth S., McDonald S., Jagels K., Annes K., Jones L., Jones M., Leather S., McDonald S., McLean J., R. Mooney P., Moule S., Mungall K., Murphy L., Miblet D., Odell C., R. A. Ollver K., O'Neil S., Saunders D., Seeger K., Sharp S., As Cliver K., O'Neil S., Saunders D., Seeger K., Sharp S., Arlor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Arlor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Weltjons I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., A Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., A Galibert F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.M., Galibert F., Aves S.J., Noreno S., Lelaure V., Mottier S., R. Galibert F., Aves S.J., Noreno S., Armstrong J., Forsburg S.L., R. Dominguez A., Revuelta J.L., Moreno S., Market D., Thode G., R. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., R. Bhakovski G.V., Ussery D., Barrell B.G., Nurse P., Harther A., R. Harther B., M. Harth
Pfam; PF00156; Pribosyltran; 1.
TIGREAMs; TIGR01091; upp; 1.
Transferase; Glycosyltransferase; Magnesium; Complete proteome.
DOMAIN 127 139 PREP-BINDING (BY SIMILARITY).
DOMAIN 193 201 UMP-BINDING, URACIL PART (BY SIMILARITY).
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = ADP + thymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abaigar L.T., Yeh Y.I., Jong A.Y., "Functional and structural conservation of Schizosaccharomyces pombe dTMP kinase gene.";
                                                                                                                                                                                                                                              .
                                                                                                                                                                                       Length 209;
                                                                                                                                                           5'-diphosphate.
-!- PATHWAY: Biosynthesis of dTTP from dTMP.
-!- SIMILARITY: Belongs to the thymidylate kinase family.
                                                                                                                                      457C6810A3651564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dIDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Catalyzes the conversion of dTMP to dTD
-!- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
TMP OR SPCC70.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim, Biophys. Acta 1132:222-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE=93003330; PubMed=1327149;
                                                                                                                                      209 AA; 23037 MW;
                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                 :|||::|:
125 REFIVVDP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P36590; 074528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTHY SCHPO
                                                                                                                                    SEQUENCE
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   KTHY SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
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EMBL; L33462; AAC41483.1; -.
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                                                                                                                          R EMBL; AL023794; CAA19357.1; -
R EMBL; AL023794; CAA19357.1; -
R PIR; $28955; $28955
R PIR; $28955; $28955
R PIR; $28955; $28955
R PIR; TAISS3; TA1553
R HSSP, P00572; 1TMK.
R GeneDB SPombe; SPCC70.07c; -.
R Flam; PF0223; Thymidylate kin; 1.
R Pfam; PF0223; Thymidylate kin; 1.
R PGATE; PS01331; THYMIDYLATE KINSE; 1.
R PROSITE; PS01331; THYMIDYLATE KINSE; 1.
R PROSITE; PS01331; THYMIDYLATE KINSE; 1.
R PROSITE; PS01331; THYMIDYLATE KINSE; 1.
R POTENTAL)
T CONFILCT 33 39 SQHEKAE - INMKELK (IN REF. 1).
T CONFILCT 59 SP3 TIQYINGUT -> PSIYYRANQORCN (IN REF. 1).
T CONFILCT B0 93 TIQYINGUT -> PSIYYRANQORCN (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant of Helicobacter mustelae.";
Infect. Immun. 63:3718-3721(1995).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBUNIT: CONSIST OF TWO SUBUNITS (ALPHA AND BETA).
-!- CAUTION: IN HELICOBACTER THE ALPHA SUBUNIT IS WHAT IS KNOWN, IN OTHER BACTERIA AS THE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=NCTC 12032;
BEDLINE=95369940; PubMed=7642313;
Solnick J.V., Josenhans C., Tompkins L.S., Labigne A.;
"Construction and characterization of an isogenic urease-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 1; Length 210; red. No. 2.3e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            4266144AEDAB68C0 CRC64;
                                                                                                                                                                                                                                                                                                                                    F -> T (IN REF. 1).
F -> L (IN REF. 1).
S -> YA (IN REF. 1).
H -> D (IN REF. 1).
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              24249 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                 EMBL; X65868; CAA46698.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter mustelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||::|:
LEFITLDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urease alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                              210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                         125
164
186
191
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CONFLICT
CONFLICT
SEQUENCE
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01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable glutathione S-transferase (EC 2.5.1.18) (Pathogenesis-related protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Taylor J.L., Fritzeneier K.H., Haeuser I., Kombrink E., Rohwer F., Schroeder M., Strittmatter G., Hahlbrock K.;

Schroeder M., Strittmatter G., Hahlbrock K.;

"Structural analysis and activation by fungal infection of a gene encoding a pathogenesis-related protein in potato.";

Mol. Plant Microbe Interact. 3:72-77(1990).

-! CATALYTIC ACTIVITY: Rx + glutathione = HX + R-S-glutathione.

-! INDUCTION: By fungal infection.

-! SIMILARITY: Belongs to the GST superfamily. HSP26 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
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InterPro; IPR004045; GST_Nterm.
Pfam; PP00043; GST_C; 1.
Pfam; PP02798; GST_N; 1.
Plant defense; Transferase; Pathogenesis-related protein.
SEQUENCE 217 AA; 25056 WW; 7B0DBBE216685B4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 21 clarity 50.0%; Pred. No. 2.3e+02; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 25; DB 1; Length 21
Pred. No. 2.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                1
213 AA; 23794 MW; B97A6A3FD2CB2F40 CRC64;
HSSP; P41022; 1UBP.
HAMAP, MF 00739; Used; 1.
InterPro; IPR002019; Urease beta.
InterPro; IPR002025; Urease_gamma.
InterPro; IPR003233; Urease_gammabeta.
Pfam; PF0059; Urease_beta; 1.
Pfam; PF00547; urease_gamma; 1.
ProDom; PD002326; Urease_gammabeta; 1.
ProDom; PD002326; Urease_beta; 1.
                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00192; urease_beta; 1.
TIGRFAMS; TIGR00193; urease_gam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J03679; AAA68430.1; -. PIR; T07595; T07595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||::|:
97 GEFILKDE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX 8
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                       Hydrolase.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MBDLINE-98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
-!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; first
                                                                                                                                                              28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase) (UMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_01220; -; 1.
InterPro; IPRO01048; Aa kinase.
Pfam; PF00696; aakinase; 1.
Transferase, Kinase, Pyrimidine biosynthesis; Complete proteome.
SEQUENCE 219 AA; 23398 MW; 751B894ED5261B91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 1; Length 219; 50.0%; Pred. No. 2.4e+02; ative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the UMP kinase family.
                                                                                                                                    219 AA
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                      Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000962; AAB89213.1; -.
                                                                                                                                  STANDARD;
                     :|||::|:
29 YEFIEEDL 36
1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A69505; A69505.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                 PYRH OR AF2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; AF2042
                                                                                                                              PYRH ARCFU 028237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence, genomic organization of the BcoRI-A fragment of Autographa californica nuclear polyhedrosis virus, and identification of a viral-encoded protein resembling the outer capsid protein VPB of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 202:586-605(1994).
-!- FUNCTION: This protein is required for viral late gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90264832; PubMed=2189022; O'Reilly D.R., Passarelli A.L., Goldman I.F., Miller L.K.; O'Reilly D.R., Passarelli A.L., Goldman I.F., Miller L.K.; Characterization of the DA26 gene in a hypervariable region of the Autographa californica nuclear polyhedrosis virus genome."; J. Gen. Virol. 71:1029-1037(1990).
                                                                                                                                                                                                                                                           Guarino L.A., Summers M.D.; "Functional mapping of Autographa california nuclear polyhedrosis virus genes required for late gene expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93079853; PubMed=1333113;
Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
Summers M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94103173; PubMed=8030224; Ayres M.D. Howard S.C., Kuzio J., Lopez-Ferber M., Possee R. "The complete DNA sequence of Autographa californica nuclear polyhedrosis virus";
                                                                                                                    Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; Length 22 50.0%; Pred. No. 2.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA; 25910 MW; D27965D85B2C7980 CRC64;
                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                            MEDLINE=88091055; PubMed=2826808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 191:1003-1008(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22619; AAA69846.1; -. EMBL; M18857; AAA66808.1; -. EMBL; M96361; AAA66786.1; -. EMBL; L22858; AAA6646.1; -.
                                                                                                                                                                                                                                                                                                                 Virol. 62:463-471(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                   Early 25.9 kDa protein.
                                                                                                                                                   Nucleopolyhedrovirus.
NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||::|:
195 FEFINPDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A29891; WMNV29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 XEFIXXDX 8
                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rotavirus."
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=L1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C6;
                                                                                                                                                                                                          SEOUENCE
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Gaps

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4; Conservative

Matches

124 AEFIKADV 131

RESULT 30 VE26_NPVAC

1 XEFIXXDX 8

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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=963-9999; Dubmd=8688089;

Bult C.J., White O., Olsen G.J., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Tomb J.P., Adams M.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
-!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
AT2G26970 OR T20P8.2.
ATABATOGS TABLIANA (Mouse-ear cress).
BLWATYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_01220; -; 1.
InterPro; IPR001048; Aa kinase.
Pfam; PF00596; aakinase; 1.
Transferase; Kinase; Pyrimidine biosynthesis; Complete proteome.
SEQUENCE 226 AA; 24099 MW; 7052087EE2AE240D CRG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Catalyzes the phosphorylation of UMP to UDP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Score 25, DB 1; Length 226;
Pred. No. 2.5e+02;
4; Mismatches 0; Indels
                                                                                                                                                          Archaea, Euryarchaeota, Methanococci, Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the UMP kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67566; AAB99262.1; ALT_INIT.
                                                                01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                Methanococcus jannaschii.
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AEFINADL 137
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                                                                                                                                                                                          NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                 PYRH OR MJ1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MJ1259
                                                                                                                                                                                                                                                                                                                                                                                         jannaschii.
                                 PYRH METJA
Q586<u>5</u>6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORN ARATH
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                        PYRH_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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        RESULT 31
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Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Qin Z.-Q., Miao Y.-G., wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.,

"Genome-based analysis of virtulence genes in a non-biofilm-forming

Staphylococcus epidermidis strain (APCC 12228) .",

Mol. Microbiol. 49:1577-1593(2003)

-!-FUNCTION: Transforms pimelate into pimeloyl-CoA (By similarity).

-!- CHTALYTIC ACTIVITY: ATP + 6-carboxyhexanoate + CoA = AMP +

diphosphate + 6-carboxyhexanoyl-CoA.

-!- COPACTOR: Magnesium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8CTZ3;
10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
6-carboxyhexanoate--CoA ligase (EC 6.2.1.14) (Pimeloyl-CoA synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                              STRAIN=CV. Columbia.
STRAIN=CV. Columbia.
MEDLINE=2003487; PubMed=10617197;
MEDLINE=2003487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lini X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Bujli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.D., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:-FINCTION: 3'-to-5' exoribonuclease specific for small oligoribonucleotides (By similarity).
-:- SIMILARITY: Belongs to the oligoribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; Length 22 50.0%; Pred. No. 2.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Hydrolase; Exonuclease; Nuclease. ACT SITE 148 148 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7126263D1E53D80E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B84667; B84667.
InterPro; IPR006055; Exonuclease.
Pfam; PF00929; Exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC005623; AAC77855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AA; 25737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 50.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00479; EXOIII; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 LEFISSĎI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 XEFIXXDX 8
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STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1282;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOW OR SE0182
                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOW_STAEP
ID BIOW_STAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT SITE
SEQUENCE
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us-09-660-302e-1.rsp

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THEMA
                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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                                                                                                                                                                                                             D9WZL2;
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TIGR;
                                                                                                                                                                  THEMA
                                                                                                                                                                                       UBIE
                                                                                                                                            RESULT 35
UBIE_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
-! PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
-! SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
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                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 228; 50.0%; Pred. No. 2.58+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                           ; Score 25; DB 1; Length 229;
Pred. No. 2.5e+02;
4; Mismatches 0; Indels
  PATHWAY: Bioconversion of pimelate into dethiobiotin.
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229 AA; 25194 MW; E6DDE60481159023 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 AA.
                      SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the biow family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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InterPro; IPR001034; HTH_DeoR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE010232; AAL81382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00455; deoR; 1.
ProDom, PD005813; RpiA, 1.
TIGRFAMS; TIGR00021; rpiA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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LEFIKNDI 101
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPIA OR PF1258.
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QBUIFO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isomerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
SETALINE=99287316; Pubmed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399:323-329(1999).
-!- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: Sadenosyl-L-methionine + demethylmenaquinol s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAX: Menaquinone biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                      Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 22
50.0%; Pred. No. 2.5e+02;
ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                            229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_01813; -; 1.
InterPro; IPR001601; Methyltranef.
InterPro; IPR001601; SAM bind.
InterPro; IPR004033; UbiE/COG5_Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE_1; FALSE_NEG.
PROSITE; PS01184; UBIE_2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001745; AAD35835.1; -.
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                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                       15 LEFIEDDM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||::|:
94 GEFIVGDA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G72337; G72337.
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1 XEFIXXDX
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SEQUENCE 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxiD=2336;
                                                                                                                                                                                                                                                                                                                                                                                                             JBIE OR TM0753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TM0753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
YP07_MYCTU
ID YF07_MYCTU
AC P71786;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
              NCBI TaxiD=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHEL_WCMVM
ID VHEL_WCMVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potexvirus
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                         Ω.
                                                                                                                                                                      MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Cole S.T., Englmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Easham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Osborne J., Skelton S., Squares S., Senger B., States R., Shalton S., Squares S., Suares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                           PETRAIN=CDC 1551 / Oshkosh;
MBDLINE=2226644; PubMed=1218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eaft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.,
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist, Rv1507c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 231 AA; 27090 MW; BD18A247DB1B0BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1;
50.0%; Pred. No. 2.5e+02;
iive 4; Mismatches 0;
                      01-NOV-1997 (Rel. 35, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv1507c/MT1555.
RV1507C OR MT1555 OR MTCY277.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007023; AAK45820.1; -. PIR; F70713; F70713.
TIGR; MT1555; -.
          01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                        complete genome sequence.";
Nature 393:537-544(1998).
                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z79701; CAB02021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PRI).
RPIA OR CCA00632.
Chlamydophila caviae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 DEFITYDD 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                   STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPIA CHLCV
Q822P7;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 -:- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
-:- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
-:- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
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STRAIN=GPIC;
MEDINE=2299155; PubMed=12682364;
MEDINE=2299155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
                                                                                                                                                                                                                                   GPIC):
                                                                                                                                                                                                                                                                   examining the role of niche-specific genes in the evolution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88124202; PubMed=3340527;
Forster R.L.S., Bevan M.W., Harbison S.-A., Gardner R.C.;
"The complete nucleotide sequence of the potexvirus white clover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                   "Genome sequence of Chlamydophila caviae (Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; Length 233; 50.0%; Pred. No. 2.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C0EDB3474B20A0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MMR-1989 (Rel. 10, Created)
01-MMR-1989 (Rel. 10, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Probable helicase (ORF 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White clover mosaic virus (strain M) (WCMV)
                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 31:2134-2147(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00170; -; 1.
InterPro; IPR004788; RpiA.
ProDom; PD005813; RpiA; 1.
Isomerase; Complete proteome.
SEQUENCE 233 AA; 25544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016996; AAP05374.1; -.
TIGR; CCA00632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 EEFINTDL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=12189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mosaic virus.";
                                                                                                                                                                                                                                                                                                                  chlamydiaceae.
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SOFERENCE

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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
1-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0286 protein SS02208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96109932; PubMed=8619318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006826; AAK42378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, C90390; C90390.
HAMAP; MF_00722; -; 1.
InterPro; IPR002793; DUF91.
                                                                            Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:
224 LEFIRYDI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
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                                                                                                                      NCBI_TaxID=2287;
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                                                                                                          Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNM9 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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YEAST
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 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REQUIRED FOR REPLICATION OF VIRAL DNA. SIMILARITY: TO ORF2 FROM OTHER POTEXVIRUSES AND TO 25 KDa PROTEIN FROM CARLAVIRUSES.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Infectious transcripts and nucleotide sequence of cloned cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potexvirus white clover mosaic virus.";
Virology 177:152-158(1990).
-!- FUNCTION: THIS PROTEIN MAY BE AN ATP-DEPENDENT HELICASE AND IS
                                                                                                                                                                                            .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDINE=90281578; PubMed=2353451;
Beck D.L., Forster R.L.S., Bevan M.W., Boxen K.A., Lowe S.C.,
Gardner R.C.;
                                                                                                                                                           100.0%; Score 25; DB 1; Length 236; 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 236; 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000666; Viral helicasel.
Pfam; PF01443; Viral helicasel; 1.
DNA replication; ATP-binding; Helicase.
NP BIND 28
SEQUENCE 236 AA; 26451 MW; D470D75B46E9D418 CRC64;
                                                                                                                               49991932D8B6D4BB CRC64;
                                            01-APR-1990 (Rel. 14, Last sequence update) 01-OCT-1993 (Rel. 27, Last annotation update) Probable helicase (ORF 2).
White clover mosaic virus (strain O) (WCWV).
                                                                                                                                                                                                                                                                                                                           236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 AA.
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             or send an email to license@isb-sib.ch)
                                                                                                                            236 AA; 26356 MW;
                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
                                         EMBL; X06728; CAA29905.1; -.
                                                                                                                                                                         50.08;
entities requires a license
                                                                                                                                            Query Match
Best Local Similarity 50.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X16636; CAA34629.1;
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                    : | | | :: | :
95 FEFIFTDP 102
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FEFIFTDP 102
                                                                                                                                                                                                                     1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=12190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 40
YMO8 SULSO
ID YMO8 SULSO
AC Q97WK8;
                                                                                                                                                                                                                                                                                                                      VHEL WCMVO
                                                                                                                                                                                                                                                                                                                                                                                                                                          Potexvirus
                                                                                                                           SEQUENCE
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VHEL WCMVO
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                                                                                                                                                               SEQUENCE FROM N.A.

STRAIREATCC 35092 / DSM 1617 / P2;

STRAIREATCC 35092 / DSM 1617 / P2;

SHEDINE=2133295; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Nall. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
mP22, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
4. Hypothetical 27.7 Rba protein in CPTI-SPC98 intergenic region.
VNL129W OR N1219 OR N1870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 1; Length 23
Pred. No. 2.6e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01939; DUF91; 1.
ProDom; PD013521; DUF91; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 236 AA; 27264 MW; 6930125F102BBAC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 AA.
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"Molecular characterization of the mitochondrial DNA of a new stopper mutant ER-3 of Neurospora crassa.";

Genetics 120:935-945(1988)

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory

chain that catalyzes the reduction of oxygen to water. Subunits 1-

3 form the functional core of the enzyme complex. Subunit 2

transfers the electrons from cytochrome c via its binuclear copper

A center to the binnetalic center of the catalytic subunit 1.

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83054012; PubMed=6291999; van den Boogaart P., van Dijk S., Agsteribbe E.; "The mitochondrially made subunit 2 of Neurospora crassa cytochrome aa3 is synthesized as a precursor protein."; FEBS Lett. 147:97-100(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c + 2 H(2)0.
COFACTOR: Copper A.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; Length 24 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cytochrome oxidase subunit 2 gene in Neurospora crassa
                                                                                                                                                                                                                                                                                                                      SEQUENCE 240 AA; 27689 MW; F04E99885774CF53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome c oxidase polypeptide II (EC 1.9.3.1) COX2 OR OXII.
                                                                                                                                                                                                                                           InterPro; IPR000764; Uridine kin.
PRINTS; PR00988; URIDINKINASE.
Hypothetical protein; ATP-binding.
ATP BIND
13 20 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 258:13230-13235(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=84032555; PubMed=6313689;
Macino G., Morelli G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89137935; PubMed=2976009;
                                                                                                                                                  EMBL; Z46843; CAA86896.1; -. EMBL; Z71405; CAA96011.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                          GermOnline; 143135; -. SGD; S0005073; YNL129W.
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213 KEFINDDD 220
                                                                                                                                                                                         PIR; S55154; S55154.
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                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986
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                                                                                                                                                                          EMBL; K00825; AAA31959.2; -.

EMBL; J01429; -; NOT_ANNOTATED_CDS.

EMBL; J01429; -.

EMBL; AG6479; CAA32813.1; -.

InterPro; IPR001505; Copper_CuA.

InterPro; IPR001405; Cyt_c_ox_2.

InterPro; IPR002429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.

Pfam; PF00116; COX2 TM; 1.

PRINTS; PR01166; CYCOXIDASEII.

PROSOTTE; PS000131; COpper_CuA; 1.

PROSOTTE; PS00078; COX2; TM; 1.

ROSOTTE; PS00078; COX2; TM; 1.
                                                                                                                                                                                                                                                                                                                                                                                               Electron transport; Respiratory chain.

DOMAIN 1 39 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
COPPER A (PROBABLE).
COPPER A (PROBABLE).
            SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97313264; PubMed=9169868;
Detrich F.S., Wulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96086928; PubMed=7500933;
Hirayama T., Maeda T., Saito H., Shinozaki K.;
Cloning and characterization of seven cDNAs for hyperosmolarity-
responsive (HOR) genes of Saccharomyces cerevisiae.";
Mol. Gen. Genet. 249:127-138(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL MATRIX (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 1; Length 250;
Pred. No. 2.7e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75854A38EF16D506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPPER A (PROBABLE)
COPPER A (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GPP2 OR HOR2 OR YER062C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 AA
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
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59
76
97
250
220
224
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STRAIN=S288c / AB972;
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137 DEFIEFDS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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GPP2_YEAST
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65 DEFIEIDL 72
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                                                                                                                              similarity).
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Q8VLE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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          Dp
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0
                                                                                                              PARTIAL SEQUENCE, FUNCTION, AND CHARACTERIZATION.
MEDLINE=96278827; PubMed=8662716;
Norbeck J., Pachlaman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlaman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlaman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlaman A.-K., Akhtar N., Blomberg A., Adler L.;
Dl.glycerol-3-phospharase from Saccharomyces cerevisiae.
Identification of the corresponding GPP1 and GPP2 genes and evidence for osmotic regulation of Gpp2p expression by the osmosensing mitogen-activated protein kinase signal transduction pathway.";
J. Biol. Chem. 271:13875-13881(1996).
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petell F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."; Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                     SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Cytoplasmic.
INDUCTION: By osmotic stress.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS DOGI, DOG2, GPP1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 25; DB 1; Length 250; Pred. No. 2.7e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0000121; F:glycerol-1-phosphatase activity; IDA. GO; GO:0005975; P:carbohydrate metabolism; IDA. GO; GO:0005114; P:glycerol biosynthesis; IMP. GO; GO:0005970; P:response to osmotic stress; IDA. InterPro; IPR006402; HAD-SF-IA-v3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27814 MW; D69F343B10417313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Mollicutes, Acholeplasmatales,
Acholeplasmataceae, Phytoplasma.
NCBI_TaxID=72989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00702, Hydrolase, 1.
TIGRFAMs, TIGR01509, HAD-SF-IA-v3; 1.
Hydrolase, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
MEDLINE=22140588; PubMed=12144771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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EMBL; U18813; AAB64598.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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GermOnline; 139142; -.
SGD; S0000864; HOR2.
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233 VEFIFDDY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S0000864; HOR2.
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28-FEB-2003
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TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS3 ALDYE
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IN 3 ALDYE
IN 28-FE
DT 28-FE
DT 28-FE
DT 28-FE
DT 28-FE
DT 28-FE
ON 28-FE
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Martini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A., Benedetti R., Bertaccini A.;
Benedetti R., Bertaccini A.;
"Genetic variability among flavescence doree phytoplasmas from different origins in Italy and France.";
Mol. Cell. Probes 16:197-208(2002).
-!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=E.w.phytoplasma, and E.y.phytoplasma; STRAIN=ULW, and EY1; MEDLINE=22140589; PubMed=12144771; Marzachi C., Casati P., Bianco P.A., Marchini M., Bottiscini A., Marchini A., Bertaccini A., "Genetic variability among flavescence doree phytoplasmas from different origins in Italy and France."; "Month of the Special Probes 16:197-208 (2002).

-: FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                      subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                            -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight cowith proteins 510 and 514 (By similarity).
-!- SIMILARITY: Belongs to the 53P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
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Elm yellows phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; 50.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.7e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF396936; AAL5724.1; -. HAMAP: MF 01309; -; 1. InterPro; IPR004087; KH dom. InterPro; IPR0040919; KH prok. InterPro; IPR001919; KH prok. InterPro; IPR001351; Ribosomal S3 C. InterPro; IPR0018282; Ribosomal S3 C. InterPro; IPR005704; S3 bact. Pfam; PF00189; Ribosomal S3 C. InterPro; IPR005704; S3 bact. Pfam; PF00418; Ribosomal S3 C; 1. Pfam; PF00418; Ribosomal S3 C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acholeplasmataceae; Phytoplasma.
NCBI_TaxID=182216, 35774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA; 28367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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NCBI_TaxID=72996;
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46
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                          HAMAP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 47
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profile institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ALL202, AT4, FD70, FD88, PC2, FN6, FV259, TV46, TV51, and VR2;
STRAIN-ALL202, AT4, FD70, FD88, PC2, FN6, FV259, TV46, TV51, and VR2;
MEDLINE-22140588; DubMed=12144771;
Martini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A.,
Benedetti R., Bertaccini A.;
"Genetic variability among flavescence doree phytoplasmas from
"Genetic variability among flavescence doree phytoplasmas from
"Genetic variability among flavescence doree phytoplasmas from
"Genetic variability among flavescence";
"Genetic variability among flavescence";
MOI. Cell. Probes 16:197-208(2002).
-:- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex with proteins 310 and 314 (By similarity).

with Belongs to the S3P family of ribosomal proteins.

-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.

-!- SIMILARITY: Concains 1 KH type-2 domain.
                subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight con with proteins S10 and S14 (Bs similarity).
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 25
50.0%; Pred. No. 2.70+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           PFam; PF00411; .....
SMART; SM00322; KH; 1.
TGRPAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS00548; KH TYPE 2; 1.
PROSITE; PS00548; RIBOSOMĀL S3; 1.
Ribosomal protein; RNA-binding.
RKH TYPE 2.
111 KH TYPE 2.
111 A TYPE 2.
111 A TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Phytoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS3_FLADO
Q8VL42; Q8VL25; Q8VL43; Q8VS62;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
                                                                                                                                                                                                                                                           InterPro; IPR009019; KH_Drok.
InterPro; IPR004044; KH_TYPE.
InterPro; IPR001351; Ribosomal S3 C.
InterPro; IPR008282; Ribosomal S3 N.
InterPro; IPR008704; S3 bact.
Fram; PF00189; Ribosomal S3 C, 1.
Pfam; PF00189; Ribosomal S3 C, 1.
                                                                                                                                                                                                  EMBL; AF396949; AAL57337.1; -. EMBL; AF396938; AAL57326.1; -. HAMAP; MF_01309; -; 1. InterPro; IPR004007; KH_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavescence doree phytoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30S ribosomal protein S3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0 les 4; Conservative
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DEFIEIDL 72
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       similarity)
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ID RS3 F
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Martini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A.,
Benedeti R., Bertaccini A.;
Genetic variability among flavescence doree phytoplasmas from
different origins in Italy and France.";
Mol. Cell. Probes 16:197-208(2002).
-: FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
-: FUNCTION: Binds prositioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 46 H -> Y (IN STRAINS AL202, AT4 AND PV259)

103 103 V -> I (IN STRAINS AL202, AT4, FD70 AND PV259)

118 118 V -> I (IN STRAINS TV46 AND TV51).

250 AA; 28408 MW; E5441C224F164FF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 1; Length 25
Pred. No. 2.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubus stunt phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Phytoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; Frvor...

SMART; SM0022; KH; 1.

TIGRFAMS; TIGR01009; FpSC_bact; 1.

PROSITE; PS50823; KH TYPE 2; 1.

PROSITE; PS00548; RIBOSOWAL, S3; 1.

Ribosomal protein; RNA-binding; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPSC OR RPS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001351; Ribosomal S3 C. InterPro; IPR001351; Ribosomal S3 N. InterPro; IPR005704; S3 bact. Pfam; PF00189; Ribosomal S3 C; I. Pfam; PF001417; Ribosomal S3 C; I.
                                                                                                                                                                                                                     EWBL, AF396937, AAL57325.1; --
EWBL, AF396939, AAL57327.1; --
EWBL, AF396942, AAL57328.1; --
EWBL, AF396942, AAL57330.1; --
EWBL, AF396943, AAL57331.1; --
EWBL, AF396944, AAL57333.1;
EWBL, AF396947, AAL57333.1;
EWBL, AF396947, AAL57335.1; --
EWBL, AF396950, AAL57335.1; --
EWBL, AF396950, AAL57336.1; --
EWBL, AF396950, AAL57336.1; --
EWBL, AF396951, AAL57338.1; --
EWBL, AF396951, AAL57338.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004087; KH dom.
InterPro; IPR009019; KH prok.
InterPro; IPR004044; KH_TYPE_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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65 DEFIEIDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !AMAP; MF_01309; -; 1
InterPro; IPR004087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XEFIXXDX 8
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us-09-660-302e-1.rsp

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Benedetti R., Bertaccini A.,
Genetic variability among flavoscence doree phytoplasmas from
"Genetic variability among france.",
"Genetic variability among france.",
Mol. Cell. Probes 16:197-208(2002).
"-- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
in the 70S ribosome, positioning it for translation (By
SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
               with proteins S10 and S14 (By similarity).
SIMILARITY: Belongs to the S3P family of ribosomal proteins.
SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with proteins S10 and S14 (By similarity). SIMILARITY: Belongs to the S3P family of ribosomal proteins. SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      E5440DD24F164FF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ziziphus jujube witches'-broom phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Phytoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                    SMAKL; SMUGAZE, AM, T.
TIGREAMS, TIGRO1009; TRSC bact; 1.
PROSITE; PSS0823; KH TYPE_2; 1.
PROSITE; PS00548; KIBOSOMĀL, S3; 1.
Ribosomal protein; RNA-bindīng; rRNA-binding.
DOMAIN 39 111 KH TYPE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                      HAMAP; MF 01309; -; 1.
InterPro; IPR004087; KH dom.
InterPro; IPR004081; KH TYPE 2.
InterPro; IPR004044; KH TYPE 2.
InterPro; IPR001351; Ribosomal S3 C.
InterPro; IPR005704; S3 bact.
Pfam; PF00189; Ribosomal S3 C.
Pfam; PF00189; Ribosomal S3 C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22140588; PubMed=12144771;
                                                                                                                                                                                         EMBL; AF396944; AAL57332.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA; 28435 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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                                                                                                                                                                                                                                                                                                                                             SMART; SM00322; KH; 1.
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DEFIEIDL 72
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SEQUENCE FROM N.A.
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QBVS61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=JWB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                        Length 250;
    as its content
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                     778D51D0B57AA2A4 CRC64;
                                                                                                                                   InterPro; IRR004044; KH TYPE 2.
InterPro; IPR004044; KH TYPE 2.
InterPro; IPR004824; Ribosomal S3 C.
InterPro; IPR005824; Ribosomal S3 N.
InterPro; IPR005704; S3 bact.
Pfam; PF00189; Ribosomal S3 C; 1.
Pfam; PF00417; Ribosomal S3 N; 1.
SMART; SM0032; KH; 1.
IGRPAMS; TIGR01009; rpsc bact; 1.
PROSITE; PS50823; KH TYPE 2; 1.
PROSITE; PS00548; RIBOSOMAL S3; 1.
Ribosomal Protein; RMA-binding; rRNA-binding.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 1; L
Pred. No. 2.7e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
COX2 OR OXIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
non-profit institutions as long
                                                                            EMBL; AF396941; AAL57329.1; -.
                                                                                                                                                                                                                                                                                                                                     28362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                     100.0%;
50.0%; F
                                                                                                            InterPro; IPR004087; KH dom.
InterPro; IPR009019; KH_prok.
                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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DEFIEIDL 72
                                                                                                                                                                                                                                                                                                                                    SEQUENCE 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
                                                                                             MF 01309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 H(2)0.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
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DPHB OR SSO0953
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Briaseppi G., Guy B.J., Hanga K., Halloh S.D., Emmerson P.T.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Garadi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hibert H., Holsappel S., Hosono S., Halloh M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B., Kostler P., Koningstein G., Krogh S., Kumano M.,

RA Nuita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Meina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroete R., Scoffone F.,

RA Stever, M., Taevoni E., Takagi T., Takabashi H., Takematu K.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tamakoshi A., Taramakoshi A., Taramakoshi A., Taramakoshi A., Takagi T., Takagi T., Taramakoshi A., Takagi T.,

RA Takeuchi M., Tamakoshi A., Taramakoshi A., Takagi T., Takagi T., Takagi T.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Taramaka P., Tooponi A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Pather R., Vansarotti A.,

RA Tosato V., Uchiyama S., Vandenelle R., Vansarotti A.,

RA Tosato V., Uchiyama S., Wedler E., Wedler F., Vansarotti A.,

RA Viazi A., Wandutt R., Wedler E., Wedler F., Vansarotti A.,
                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL MATRIX (POTENTIAL).
POTENTIAL.
MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
COPPER A (PROBABLE).
                 InterPro; IPR001505; Copper_CuA.
InterPro; IPR008922; Cupredoxin.
InterPro; IPR008922; Cupredoxin.
InterPro; IPR008922; Cupredoxin.
Pfam; PF00116; COX2; 1.
Pfam; PF00116; COX2 TM; 1.
PRINTS; PR01166; CYCOXIDASEII.
PROSITE; P8000131; Copper_CuA; 1.
PROSITE; P800078; COX2; II.
Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-WAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical protein yoxB (ORF119+).
                                                                                                                                                                                                                                      Respiratory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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(Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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  EMBL; X15441; CAA33481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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105
252
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                                                                                                                                                                                                                                         Electron transport;
                                                                                                                                                                                                                                                                                  40
60
106
1106
219
223
223
252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 XEFIXXDX 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P28671; 054515;
01-DEC-1992 (Rel
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TRANSMEM
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STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=21312959; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S. A. 98:7835-7840(2001).

-: FUNCTION: Required for the methylation step in diphthamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequence analysis of the Bacillus subtilis chromosome region between the terC and odhAB loci cloned in a yeast artificial chromosome."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                          Ann K.S., Wake R.G.; "An Avariations and coding features of the sequence spanning the replication terminus of Bacillus subtilis 168 and W23 chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; Length 25
50.0%; Pred. No. 2.8e+02;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B69930; B69930.
Subtilist; BG11046; yoxB.
Hypothetical protein; Complete proteome.
SEQUENCE 256 AA; 28452 MW; B9B64B08ECEOAB3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M24523; -; NOT ANNOTATED CDS.
EMBL; AF027868; AAB84418.1; -.
                                                                                                                                                                                                                                                                                                                                 MEDLINE=91192601; PubMed=1849493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 72-256 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99114; CAB13745.1; -.
                                                                                                                                                                                                                                                      SEQUENCE OF 1-119 FROM N.A.
                                                                                                                                                                           Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 98:107-112(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||:||
48 NEFINRDA 55
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Kim S.-H.;
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STRAND
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P SEQUENCE FROM N.A.

RX MEDLINE=1154948; PubMed=11677609;

RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Curtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., RA Pyan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium "Complete genome sequence of Salmonella enterica serovar Typhimurium "T."
                                                                                                                                                                                                                                                                                                                                                                       Gaps
biosynthesis (By similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = 3-adenosyl-L-homocysteine + 2-[3-carboxy-3-arboxy-3-(methylamonio)propyl]-L-histidine.
PATHWAY: Diphthamide biosynthesis; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=82082392; PubMed=6273842;
Higgins C.F., Ames G.F.-L.;
"Two periplasmic transport proteins which interact with a common membrane receptor show extensive homology: complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LO-CEM-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Lysine-arginine-ornithine-binding periplasmic protein precursor
(LAO-binding protein).
ARGT OR SIM2355.
                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92084686; PubMed-1748660;
Kang C.-H., Shin W.-C., Yamagata Y., Gokcen S., Ames G.F.-L.,
Kim S.-H.,
                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 1; Length 257; Pred. No. 2.8e+02; 4; Mismatches 0; Indels
                                                                SIMILARITY: Belongs to the diphthine synthase family.
                                                                                                                                                                                                             PIR; D00246; D90246.
HAMAP; MF_01084; -; 1.
InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR0004551; Dphthn synthase.
Pfam; PF00590; TP methylase; 1.
IIGRFAMs; TIGR00522; dph5; 1.
Transferase; Methyltransferase; Complete proteome.
SEQUENCE 257 AA; 28834 MW; 218BE19B593BF01B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 78:6038-6042(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                   EMBL; AE006715; AAK41227.1; +.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium
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55 REFIEADR 62
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ARGT_SALTY
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DT 28-PEB-DT 10-OCTB-DE (LAO-DE ON ARGTO)
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                                                                                                                                                                                                                                                                                                                               Kim S. H.;
J. Biol. Chem. 268:17648-17649(1993).
-!- FONCTION: THIS PERIPLASMIC BINDING PROTEIN IS INVOLVED IN AN ARGININE TRANSPORT SYSTEM. ARGI AND HISTIDINE-BINDING PROTEIN J (HISJ) INTERACT WITH A COMMON MEMBRANE-BOUND RECEPTOR, HISP.
-!- SUBCELULIAR LOCATION: Periplasmic.
-!- SIMILARITY: Relongs to the bacterial extracellular solute-binding
                                                                               X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE-93266593; PubMed-8496186;
Oh B.-H., Pandit J., Kang C.-H., Nikaido K., Gokcen S., Ames G.F.-L.,
                                                                                                                                                                                                                                                                                                              Oh B.-H., Pandit J., Kang C.-H., Nikaido K., Gokcen S., Ames G.F.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR01096; 3A0101803R; 1.
PROSITE; PS01039; SBP_BACTERIAL_3; 1.
Transport; Amino-acid transport; Periplasmic; Signal; 3D-structure;
"Crystal structure of the lysine-, arginine-, ornithine-binding protein (LAO) from Salmonella typhimurium at 2.7-A resolution."; J. Biol. Chem. 266:23893-23899(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSINE-ARGININE-ORNITHINE-BINDING
                                                                                                                                                                             "Three-dimensional structures of the periplasmic lysine arginine/ornithine-binding protein with and without
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stydene; SG10018; argr.
InterPro; IPR005768; Lys Arg Orn bind.
InterPro; IPR001311; SBP/glu receptor.
InterPro; IPR001638; SBP bac 3.
Pfam; PF00497; SBP_bac 3; 1.
                                                                                                                                                                                                                                               Biol. Chem. 268:11348-11355(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V01368; CAA24651.1; -.
EMBL; J01805; AAA75577.1; -.
EMBL; AE008806; AAL21256.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1LST; 22-JUN-94.
PDB; 2LAO; 22-JUN-94.
PDB; 1LAF; 10-JUL-95.
PDB; 1LAG; 10-JUL-95.
PDB; 1LAH; 10-JUL-95.
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B.";
J. Biochem. 95:465-475(1984).
-: CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity,
-: CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity,
cleaving 24-Phe-1-Phe-25, but not 15-Leu-|-Tyr-16 and 25-Phe-|-
Tyr-26 in the B chain of insulin.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MISSING (IN REF. 3).
N -> D (IN REF. 3).
MISSING (IN REF. 3).
D73852833694C6E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 25; DB 1; Length 26
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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STRALM-EXL2 / MG1655,
STRALM-S513452; Pubmed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                           SIMILARITY: Belongs to peptidase family A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Aspartyl protease; Zymogen; Signal.
SIGNAL 1 20 POTENTIAL.
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Ferric iron reductase protein fhuF.
ENCH OR B4367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000250; Peptidase_A4.
Pfam; PF01228; Peptidase_A4; 1.
PRINUS; PR0097; SCYILDPTASE.
ProDom; PD018627; ASPPIOCEASEA4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB038553; BAA92164.1; -.
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Maita T., Nagata S., Matsuda G., Maruta S., Oda K., Murao S.,
Tsuru D.; "Complete amino acid sequence of Scytalidium lignicolum acid protease
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MEDLINE=98430139; PubMed=9757573;

MEDLINE=9600 N. Oyama H., Murao S., Oda K., Tsuru D.;

"Mucleotide sequence of the gene encoding the precursor protein of pepstatin insensitive acid protease B, scytalidopepsin B, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRTS SCYLI STANDARD; PRT; 260 AA.
1915369, 0293333, 029562;
01-APR-1990 (Rel. 14, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Scytalidopepsin B precursor (EC 3.4.23.32) (Acid protease B) (SLB)
Scytalidium lignicolum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Scytalidium.
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SEQUENCE OF 50-260 FROM N.A.
MEDLINE=96376187; PubMed=8782420;
Kakimori T., Yoshimoto T., Oyama H., Oda N., Gotoh Y., Oda K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 260; 50.0%; Pred. No. 2.9e+02; ive 4; Mismatches 0; Indels
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Biosci. Biotechnol. Biochem. 62:1637-1639(1998)
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46 GEFIGFDI 53
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                                                                                                                             of 2Fe-2S center. \overline{u} , Eur. J. Biochem. 258:1001-1008(1988). -!- FUNCTION: Involved in the reduction of ferric iron in cytoplasmic
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                                                                  Muller K., Matzanke B.F., Schunemann V., Trautwein A.X., Hantke K., "FhuF, an iron-regulated protein of Escherichia coli with a new type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                  COFACTOR: Binds 1 2Fe-2S cluster. SUBCELLULAR LOCATION: Cytoplasmic; sometime membrane-associated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=21015721; PubMed=11130714;
MEDLINE=21015721; PubMed=11130714;
Miyalama N., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu B.,
Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 25; DB 1; Length 26;
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; u...

EMBL; AE00500; ...

RDR; S6594.

R EcoGene; EQ1259; fhuf.

DR PRINTS; PR01714; 2FB2SRDCTASE;

MRTAL 244 244 IRON-SULFUR (2FE-2S).

RTAL 245 245 IRON-SULFUR (2FE-2S).

RTAL 245 245 IRON-SULFUR (2FE-2S).

RTAL 245 1RON-SULFUR (2FE-2S).

RTAL 245 1RON-SULFUR (2FE-2S).

RTAL 256 IRON-SULFUR (2FE-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7708E776B1BE7783 CRC64;
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                                      MEDLINE=99144129; PubMed=9990318;
Muller K., Matzanke B.F., Schunem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
50.0%; I
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Best Local Similarity
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SEQUENCE FROM N.A.
CHARACTERIZATION.
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RRS4 ARATH
ID RS4 ARATH
DT 01-FE
DT 01-FE
DT 01-FE
DT 15-MB
DB 408 rabs
OC 60c curo
OC 60c c
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Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Albabermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
Stoneking T., Pepin K., Spieth J., Schkon M., Armetrong J., Becker M.,
Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
Belter E., Muyer K., Milan J., Haakensen B., Lamar E., Latreille P.,
Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Jernell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Nirfolf K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Polckaert G., Wambut R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Diagham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Weitzenegger T., Bahrek K., Weiler E., Johnson S.,
Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Weitzenegger T., Bahch G., Rose M., Hauf J., Berneiser S., Hempel S.,
Reidpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
Schueler C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
RA Schueler C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
Rhalian R.-B., Rese M., Mayer K.F. X., Rudd S., Schoof H.,
RR Fhalian R.-B., Resh M., Mayer K.F. X., Rudd S., Schoof H.,
Rhalian R.-B., McWeller B., Roben M., Fransz P.F.;
Rhalian R.-B., McWeller B., Roben M., Fransz P.F.;
Rhalian R.-B., Roben G., Mayer K.F. X., Rudd S., Schoof H.,
Rhalian R.-B., McWeller B., Roben M., Fransz P.F.;
Rhalian R.-B., Roben G., Roben G., Chepper R., Rayen R., Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delseny M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
Philipps G., Gigot C.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., De
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Cooke R., Laudie M., Raynal M., Delseny M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:823-826(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                    | PIR; AB3961,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.coli; MEDLINE=89136010; PubMed=2645057; de Boor P.A.J., Crossley R.E., Rothfield L.I.; de Boor P.A.J., crossley R.E., Rothfield L.I.; de Advision inhibitor and a topological specificity factor coded for by the minicell locus determine proper placement of the division septum in E. coli...;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-FBE-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Septum site-determining protein minD (Cell division inhibitor minD).
MIND OR B1175 OR C1622 OR Z1937 OR ECS1669 OR SF1162 OR S1248.
Bscherichia coli 06,
Bscherichia coli 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=E.coli, STRAIN=K12 / MG1655,
MEDLINE=97426617, PubMed=9278503,
Blatturer F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacīeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Ross
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 1; Length 26
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61B8E1C557CC5485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30224 MW;
                                                                                                                                                                                                                         EMBL; AP001515; BAB06208.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 56:641-649(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 QEFIQRDN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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MIND ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- FUNCTION: Digests double-stranded RNA. Involved in the processing of ribosomal RNA precursors and of some mRNAS (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphomonoester.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
---- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
---- SIMILARITY: Contains 1 RNase III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 2125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; Nakamura Y., Maeno G., Sasaki R., Masui N., Fuji P., Hirama C., Nakamura Y., Ggasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
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P -> S (IN REF. 5).
R -> M (IN REF. 5).
A -> S (IN REF. 5).
I -> IV (IN REF. 6).
AS -> SA (IN REF. 6).
W, EF0847171FB9CA67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score ... 2.96+v
50.0%; Pred. No. 2.96+v
... 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00528; RIBOSOMAL_S4E; 1.
PROSITE; PS50889; 84; 1.
Ribosomal protein; RNA-binding.
81bosomal y 42 104 S4 RNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA
                                              or send an email to license@isb-sib.ch)
                                                                                             EMBL, AB010697; BAB11167.1; ALT_SEQ. EMBL; AY05093; AAK9350.1; -. EMBL; AY05093; AAK93510.1; -. EMBL; Z17994; CAA79086.1; ALT_INIT. EMBL; Z32619; CAA83563.1; -. EMBL; Z32619; CAA83562.1; -. EMBL; T28499; CAA79206.1; -. EMBL; T48480; T48480. InterPro; IPR005824; XOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00467; KOW; 1.
Pfam; PF00900; Ribosomal_S4e; 1.
Pfam; PF01479; S4; 1.
Probom; PD002667; Ribosomal_S4E; 1.
SMART; SM00739; KOW; 1.
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                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006646; KOW sub.
InterPro; IPR000876; Ribosomal_S4E.
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                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002942; S4.
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RNC OR RNCS OR BH2489.
Bacillus halodurans.
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170 VEFIKEDV 177
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31
53
55
92
257
262 AA;
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Matches 4; Conserv
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Q9KA05;
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Gaps

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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SPECIES=E.COli; STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S.-R., Boutin A., Hackett J., Stroud D.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

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SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-E. Coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
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MEDLINB=22590274; PubMed=12704152;
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MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
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RAPARRER REPRESENTED TO THE REPRESENTATION OF THE REPRESENTATION O
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modelist institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         division to the middle of Eacherichia coli:",
Proc. Natl. Acad. Sci. U.S.A. 96;4971-4976(1999)
-!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT IN
CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF TH
POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF TH
CELL TO DESTABILIZE FIZZ FILLAMENTS THAT HAVE FORMED BEFORE THEY
MATURE INTO POLAR Z RINGS.
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"Rapid pole-to-pole oscillation of a protein required for directing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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K->Q: LOSS OF ACTIVITY.
KT->QR: LOSS OF ACTIVITY.
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-!- SUBCELJULAR LOCATION: Inner membrane-associated.
-!- SIMILARITY: Belongs to the parA family. MinD subfamily.
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli;
MEDLINE=99238467; PubMed=10220403;
   Infect. Immun. 71:2775-2786(2003)
                                                                             SPECIES=E.coli;
MEDLINE=92097557; PubMed=1836760;
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FIR; E90837; E90837; E90837; E95595; ERS595; ERS595; ERS595; ERS595; ERS59694; E90694; E90694; E90697; COLI.
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InterPro; IPR000707; ATPase_ParA
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EMBL; D90751; BAA36091; -
EMBL; D90752; BAA360221; -
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                                                          AND MUTAGENESIS.
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RESULT 58 ILIA RAT

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MEDILINE=85240547; PubMed=2989698; March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V., March C.J., Mosley B., Larsen A., Cerretti D.P., Grabstein K., Conlon P.J., Gills S., Henney C.S., Kronheim S.R., Grabstein K., Cosman D.; Hopp T.P., Cosman D.; "Cloning, sequence and expression of two distinct human interleukin-1
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MEDLINE=86141855; PubMed=3485152;
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"Recombinant human interleukin 1 alpha: purification and biological
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MEDLINE=90249285; PubMed=2035664;
Kotenko S.V., Bulenkov M.T., Velko V.P., Epishin S.M., Lomakin I.B., Emel Yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y., Kazlov A.P., Konusova V.G., Kotov A.Y., Venthatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A., Vinetskii Y.P.,
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MEDLINE=87156769; PubMed=3493774;
Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
Nishida T., Nishina Y.,
                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-85297782; PubMed=2994016;
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Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
"Cloning and characterization of the cDNAs for human and rabbit
                (IL-1 alpha precursor (IL-1 alpha) (Hematopoietin-1)
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                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization.";
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IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE BEING IDENTIFIED AS ENDOGENOUS PROGENS. AND ARE REPORTED TO STIMULATE IDENTIFIED AS ENDOGENOUS PROGENS. AND ARE REPORTED TO STIMULATE DOWAIN: THE STIMULATIVE AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE SMINISHITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE PRECURSOR SUGGESTS THAT IL-1 PRECURSOR SUGGESTS THAT THE PRECURSOR SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS.

OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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                                                                                                                                                                                       Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                    MEDLINE=89278054; PubMed=2471704;
Nishida T., Nishino N., Takano M., Sekiguchi Y., Kawai K.,
Misuno K., Nakai S., Masui Y., Hirai Y.;
"Molecular cloning and expression of rat interleukin-1 alpha cDNA.";
J. Biochem. 105.351-357(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-1 ALPHA.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
E3BE22F576F291DE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01583; 1ITA.
InterPro; IPR001896; Cytok III like.
InterPro; IPR001896; Lil propep.
InterPro; IPR001975; Interleukin .
Pfam; PF00340; ILL; 1.
Pfam; PF00344; ILL; 2ropep; 1.
SMART; SM00125; ILI; 1.
PROSITE; PS00125; INTERLEUKIN 1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 25; DB 1; Length 270;
Pred. No. 3e+02;
4; Mismatches 0; Indels
                                                                                                   Interleukin-1 alpha precursor (IL-1 alpha).
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01, Last sequence update)
                270 AA
                                                        (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 37, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the IL-1 family.
              PRT;
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                STANDARD;
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139
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21-JUL-1986
21-JUL-1986
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ID TL1A HUMAN
                                                             01-AUG-1990
01-AUG-1990
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134

合

RESULT 59

CARBOHYD SEQUENCE CARBOHYD

PROPEP

Match

Query Best L

Matches

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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlywis S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.W., Worley M.A., Garcia A.M., Gay L.J., Hulyk S.W., A. Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., A. Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Blakealey R.W., Touchman J.W., Scheurt J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Botherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length T. Dron, Marl Marl M. Marl M. M.
                                                                                                                                                                                                                    Zsebo K.M., Wypych J.Yuschenkoff V.N., Lu H., Hunt P., Dukes P.P., Langley K.E.; Prefects of hematopoietin-1 and interleukin 1 activities on early hematopoietic cells of the bone marrow.";
                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                SEQUENCE OF 113-132.
MEDLINE=88184226; PubMed=3281727;
                                                                                                                                                                                                                                                                                                                           Satow Y.;
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MRIGYCLATION

WRIGYCLATION

WRIGHE-93346250; PubMed=8346241;

MEDLINE=93346250; PubMed=8346241;

Stevenson F.T., Bursten S.L., Fanton C., Locksley R.M., Lovett D.H.;

Stevenson F.T., Bursten S.L., Fanton C., Locksley R.M., Lovett D.H.;

The 31-kDa precursor of interleukin 1 alpha is myristoylated on specific lysines within the 16-kDa N-terminal propiece.",

Proc. Natl. Acad. Sci. U.S.A. 90:7245-7249(193).

-!- PUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE B-CELL

MATURATION & PROLIFERATION & FIRROBLAST GROWTH FACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CHERRASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS. X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). MEDLINE=92268016; PubMed=2346741; Graves B.J., Hatada M.H., Hendrickson W.A., Miller J.K., Madison V.S., "Structure of interleukin 1 alpha at 2.7-A resolution.";

DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. ANSCELLANDOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETCRY PROTEINS.

SIMILARITY: Belongs to the IL-1 family.

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EMBL, X02531; CAA26371.1; -
EMBL, X02831; CAA27448.1; -
EMBL, X0281; CAA2664.1; -
EMBL, X56086; CAA35566.1; -
EMBL, M28983; AAA59134.1; -
EMBL, AF536338; AAA96489.1; -
EMBL; BC3338; AAM96489.1; -
                                                                                                                                                EMBL; AF536338; AAM96189],; -.
EMBL; BC013142; AAH13142.1; -.
PIR; A23385; ICHUIA.
                                                                                                                                                                                                                 PDB; 2ILA; 15-0CT-92.
PDB; 1ITA; 31-0CT-93.
Genew; HGNC:5991; IL1A.
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Gaps
            GO; GO: 0005515; C: extracellular space; TAS.
GO; GO: 0005125; F: cytokine activity; TAS.
GO; GO: 0004871; F: signal transducer activity; TAS.
GO; GO: 000616; P: antl-apoptosis; TAS.
GO; GO: 0006283; P: cell proliferation; TAS.
GO; GO: 0006594; P: inflammatory response; TAS.
GO; GO: 0008285; P: p: equipartion of cell proliferation; TAS.
InterPro; IPR008996; Cytok ILI like.
InterPro; IPR003502; ILI propep.
InterPro; IPR00975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                 Pfam; PF00340; III; 1.
Pfam; PF00340; III; 1.
SMART; SMO125; IIII; 1.
PROSITE; PS00253; IIIT; 1.
CYLOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1).
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D -> H (in dbSNP:1801715).
/Frid=VAR_014601.
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/FTId=VAR_014304.
A -> S (in_dbSNP:17561).
/FTId=VAR_014305.
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                                                                                                                                                                                                                                                                                                                                                                                   N(6)-myristoyl lysine.
N(6)-myristoyl lysine.
N-LINKED (GLCNAC. ..)
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PROPEP
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132 YEFILNDA 139
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Best Local Similarity
Matches 4; Conserv
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AC P79340;
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                                                                                                                                                                                                                                 DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSOR SUGGESTIS THAT THE AMINO ENDS OF THESE PROPEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLANGOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS PRECURSOR SEQUENCE AMOUNTS NIFFERING FROM THAT USED FOR OTHER
                                                                        J. Immunol. 155:3946-3954(1995).

-!- PUNCTION: PRODUCED BY ACTIVED MACROPHAGES, IL-1 STIMULATES
-!- PUNCTION: PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
THYMOCYTE PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IL-1 PROTEINS AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Inflammatory response; Pyrogen.
BY SIMILARITY.
Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bactéria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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N-LINKED (GLCNAC. ) (.
N-LINKED (GLCNAC. ) (.
N-LINKED (GLCNAC. ) (.
N-LINKED (GLCNAC. ) (.
                                                                                                                                                                                                                                                                                                                                              OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
17yrosinase (EC 1.14.18.1) (Monophenol monooxygenase).
MELC2 OR MEL.
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4; Mismatches
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InterPro; IPR003502; ILI propep.
InterPro; IPR000975; Interleukin 1.
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                                                                      155:3946-3954 (1995)
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PROPEP 1 112 B
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Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00340; ILL; 1.
Pfam; PF02394; ILL] propep; 1.
SMART; SM00125; ILL; 1.
PROSITE; PS00253; INTERLEUKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U19844; AAA86708.1; -.
HSSP; P01583; 11TA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces lincolnensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             SECRETORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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132 HEFILNDT 139
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141 1
211 2
271 AA;
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                                                       nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=78-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                    Tatsumi M.;

submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-i- PUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE B.—CELL

MATURATION & PROLIFERATION, W. FIBROBLASCH GROWHF PACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

IL-1 PROTEINS ARE NOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE

THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

-i- SUBUNIT: MONOMER.

-i- DOWAIN: THES SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

MIND SINS OF THESE PROTEINS SERVE SOME AS YET UNDERFINED FUNCTION.

-I- MISCELLANBOUGS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE

PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL).
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Pfam; PF00340; IL1; 1.
Pfam; PF02394; IL1 propep; 1.
SMARY; SMO0125; IL1; 1.
PROSITE; PS0023; INTERLEUKIN 1; 1.
PROSITE: PS0023; INTERLEUKIN 1; 1.
PROSITE: PS0023; INTERLEUKIN 1; 1.
PROSITE: PS0023; INTERLEUKIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annocation update)
Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 271;
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N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
W, 0526A9A6404558F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3e+0
i; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the IL-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008996; Cytok III_like.
InterPro; IPR003502; III_propep.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30685 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                 SECRETORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:
132 HEFILNDT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                   SEQUENCE FROM N.A.
                     NCBI_TaxID=9541;
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CARBOHYD CARBOHYD SEQUENCE Query Match

CARBOHYD

Matches

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P48089

RESULT 61 IL1A MACMU

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Gaps

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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

(POTENTIAL)

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TYRO STRAL
P55022;
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dangy Y.-C., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Mao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228).",
Mol. Microbiol. 49:15.77-1593(2003).
-!- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + NH(3) + H(2)O = AMP
-!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: Belongs to the NAD synthesis.
                                                                           CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAQUINONE + H(2)O.
COFACTOR: Binds 2 copper ions per subunit (By similarity). SIMILARITY: Belongs to the tyrosinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 25; DB 1; Length 272;
Pred. No. 3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBCNPI, 2/5 AA. 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 143, dependent NAD(+) synthetase (EC 6.3.5.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008922; Di-Copper centre.
InterPro; IPR002627; Tyrosinase.
PERM; PR00264; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE; PROSITE; PS00497; TYROSINASE 1; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
Melanin biosynthesis; Oxidoreductase; Moi INIT MET 0 0 BY SIMILARI'
METAL 36 36 COPPER A (BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30723 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
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52
61
188
192
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37 NEFIVADT 44
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STRAIN=ATCC 12228;
PubMed=12950922;
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NADE STREE

AC QBCNF1;
DT 15-MAR-2004
DT 15-MAR-2004
DT 15-MAR-2004
DT 15-MAR-2004
DF 163 depende
GN 163 depende
GN SEIS;
OS Staphylococci
OS STATN=17,
RN [1]
RN GSTRAIN=ATCC
RX PUDMEG-12950;
RA Zhang Y.-Q.,
COIN Z.-H.,
MOIN Z.-H.,
RA YUAN Z.-H.,
CC -I-CATALYTI
CC MOIN GOODGOOG
CC -I-CATALYTI
CC -I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM 40480;
Wheneler U.F., Brass N., Roessler C., Piepersberg W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDM databases.
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAquinone + H(2)0.
-!- COFACTOR: Binds 2 copper ions per subunit (By similarity).
-!- SIMILARITY: Belongs to the tyrosinase family.
                            Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces,
                                                                                                                                                                                                                                   Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monooxygenase; Copper.
                                                                                                                                                                                                                                                                 0; Indels
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COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

COPPER B (BY SIMILARITY).

COPPER B (BY SIMILARITY).

COPPER B (BY SIMILARITY).

COPPER B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Tyrosinase (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9399BBAEFB93A173 CRC64
                                                                                                                                                                                                                            100.0%; Score 25; DB 1; 50.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002227; Tyrosinase.
Pfam; PF00264; tyrosinase; 1
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.
PROSITE; PS00498; TYROSINASE.
Melanin biosynthesis; Oxidoreductase; Mono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X95705; CAA65005.1; -.
InterPro; IPR008922; Di-copper_centre.
InterPro; IPR002227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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97 LEFINPDT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces albus G.
                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
                                                                                                                                                                                                                            Query Match
Best Local Similarity
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65
192
196
218
275 AA;
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METAL
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51
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Best Local Similarity
                                        FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ;
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ID TRMB BACTN
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                                        SECUENCE
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                                                                                                                                                                                                                                                         Hebling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + NH(3) + H(2)O = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      Gaps
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                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 1; Length 277; Pred. No. 3.1e+02;
                      ; Score 25; DB 1; Length 275; Pred. No. 3.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + NAD(+).
-!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: Belongs to the NAD synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00103; -; 1.

HAMAP; MF 00103; -; 1.

InderPro; IPR003694; NAD_synthase.

Pfam; PF02540; NAD synthase; 1.

TIGRPAMS; TIGR00552; nadE; 1.

TIGRPAMS; TIGR00562; nadE; 1.

TIGRPAMS; TIGR00562; nadE; 1.
                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)
NADE OR CGL2534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WC2B YEAST STANDARD; PRT; 278 AA. P43639; Q9URG5; 01-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Casein kinase II beta chain (CK II).
                                                                                                                                                                                                                                                                       277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005282; BAB99927.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AA; 30426 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                               100.0%;
50.0%; F
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4; Conservative
                                                                          Conservative
                                                                                                                                                                                                                                                                           STANDARD;
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38 NEFIMSDT 45
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Best Local Similarity
                                                                                                                     1 XEFIXXDX 8
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Best Local Similarity
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SEQUENCE
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GO; GO:0005956; C:protein kinase CK2 complex; IDA.

GO; GO:0006873; F:protein kinase CK2 activity; IDA.

GO; GO:0006873; F:protein kinase CK2 activity; IDA.

GO; GO:0000283; F:call ion homeostasis; IMP.

GO; GO:0000283; F:catablishment of cell polarity (sensu Sacch. . .; IPI.)

GO; GO:000082; F:GI/S transition of mitotic cell cycle; IPI.

GO; GO:0000686; F:GI/S transition of mitotic cell cycle; IPI.

GO; GO:00006469; F:protein amino acid phosphorylation; IDA.

GO; GO:0006469; P:regulation of transcription from Pol I prom. .; IDA.

GO; GO:0006599; P:regulation of transcription from Pol III pr. .; IDA.

GO; GO:0006449; P:regulation of transcription from Pol III pr. .; IDA.

R GO; GO:0006449; P:regulation of transcription from Pol III pr. .; IDA.

R GO; GO:0006447; P:regulation of transcription from Pol III pr. .; IDA.

R GO; GO:0006449; P:regulation of transcription from Pol III pr. .; IDA.

R GO; GO:0006449; P:regulation of transcription from Pol III pr. .; IDA.

R GO; GO:0006449; P:regulation of transcription from Pol III pr. .; IDA.

R FAMI, PRO1214; CK_II beta; I.

R FAMI, PRO1214; CK_II beta; I.

R FAMITS; PRO472; GASKINASE_II.
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MEDLINE=94182950; PubMed=8135547;

Bidwai A.P., Reed J.C., Glover C.V.C.;

Bidwai A.P., Reed J.C., Glover C.V.C.;

Bidwai A.P., Reed J.C., Glover C.V.C.;

Biochem kinses II of Saccharomyces cerevisiae contains two distinct regulatory submits, beta and beta.";

Arch. Biochem. Biophys. 309:348-355(1994).

-!- FUNCTION: Plays a complex role in regulating the basal catalytic activity of the alpha submit (By similarity).

-!- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one beta chain and one beta chain.

-!- FTW: Phosphorylated by alpha chain (By similarity).

-!- SIMILARITY: Belongs to the casein kinase 2 beta chain family.
                   Bidwai A.P., Reed J.C., Glover C.V.C.; 
"Cloning and disruption of CKB1, the gene encoding the 38-kDa beta 
subunit of Saccharomyces cerevisiae casein kinase II (CKII). Deletion 
of CKII regulatory subunits elicits a salt-sensitive phenotype."; 
J. Biol. Chem. 270:10395-10404 (1995).
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SEQUENCE 278 AA; 32265 MW; 9ACA8D285E6990AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 25; DB 1; Length 278; Pred. No. 3.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Hebling U., Hofmann B., Delius H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą.
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MEDLINE=95256195; PubMed=7737972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
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us-09-660-302e-1.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O., A Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B., Mayer F., Lederer H., Schuster S.C.;
A Mayer F., Lederer H., Schuster S.C.;
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Sephosphate phosphodiserter bonds at apurint are base-free deoxyribose 5-phosphate contained by the sequence of Sephosphodisentially attacks modified AP sites created by C. CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
T. COMPACTOR: Binds 3 zinc ions (By similarity).
T. SIMILARITY: Belongs to the AP endonuclease family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00152; -; 1.

PROSTIE; PS00729; AP NUCLEASE F2 1; 1.

PROSTIE; PS00731; AP NUCLEASE F2 2; 1.

PROSTIE; PS00731; AP NUCLEASE F2 3; FALSE NEG.

Hydrolase; Nuclease; Endonuclease; DNA repair; Metal-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                  Length 281;
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1 (BY SIMILARITY).
1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                              OB72FCE982FE320A CRC64;
                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Le 60.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                          EMBL; Z11874; -; NOT ANNOTATED_CDS. EMBL; X70810; CAA50077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                  PIR; 334496; S34496.
Chloroplast; Hypothetical protein.
SEQUENCE 281 AA; 33009 MW; 0B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22882897; PubMed=14500908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BX571661; CAE10776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacteraceae; Wolinella.
                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolinella succinogenes.
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110
146
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208 NEFIGVDS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSMZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            END4 WOLSU
Q7M8B4;
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 69
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=VDI-5482 / ATCC 29148;

STRAIN=VDI-5482 / ATCC 29148;

MDDIANE=22550858; PubMed=12663928;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
-!- FUNCTION: Catalyzes the formation of N(7)-methylguanine at
position 46 (M7646) in tRNA (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
homocysteine + tRNA containing N(7)-methylguanine.
-!- SIMILARITY: Belongs to the methyltransferase superfamily. TrmB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promiser, Methyltransf 4; 1.
Probom; PD000288; Aldo/ket_red; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome. SEQUENCE 280 AA; 32678 MW; 56F96C400D6CDEFI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                  Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
Bacteroidaceae, Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 25; DB 1; Length 280; Pred. No. 3.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
protein in FSBD intron 8 (ORF281A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Buglenozoa, Buglenida, Buglenales, Buglena.
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAD; MF 01057; -; 1.
InterPro; IPR001395; Aldo/ket red.
InterPro; IPR003358; Methyltransf 4.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93347989; PubMed=8346031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE016942; AA078999.1; -.
                                                                                                                                           Bacteroides thetaiotaomicron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Hypothetical 33.0 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 VEFITEDL 213
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                                                                                              methyltransferase)
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Chloroplast.
                                                                                                                                                                                                                    NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993
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Query Match

Matches

ð DP P31918;

RESULT 6
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YCX1 EDG
YCX1 EDG
DD DT 01DD DT 16DD HYI
DD HYI
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1 XEFIXXDX
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                               SEQUENCE FROM N.A.
          NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELA ACEXY P27897;
Clostridium
                                            STRAIN=13 /
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8XMY9;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Spermidine synthase (BC 2.5.1.16) (Putrescine aminopropyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                    STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPEE OR CPE0550.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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0
                                                                                                              0;
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 282;
                                                                                        Score 25; DB 1; Length 282;
Pred. No. 3.1e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 28
50.0%; Pred. No. 3.18+02;
.ive 4; Mismatches 0; Indels
    ZINC 2 (BY SIMILARITY).
ZINC 3 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 3 (BY SIMILARITY).
ZINC 3 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
W, 9C8F6FF37D50BC09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 protein; Complete proteome.
282 AA; 31331 MW; 8C9CDD6E47065445 CRC64;
                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein RC0079.
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                                                                                                     Pred. No. 3.1e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE008575; AAL02617.1; -.
                                                                      31169 MW;
                                                                                            100.08;
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                                                                                                                 Conservative
                                                                                                                                                                                                               STANDARD;
               183
217
230
232
262
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156 LEFIDKDG 163
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245 FEFIMNDP 252
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               183
217
230
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262
282 AA;
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                 4;
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092JIB;
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SPEE CLOPE
                                                  METAL
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDF-glucose pyrophosphorylase) (UDFQP) (Alpha-D-glucosyl-1-phosphate uridylyltransferase) (Uridine diphosphoglucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                  flesh-eater";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!-CATALYTIC ACTIVITY: S-adenosylmethioninamine + putrescine = 5'--
methylthicadenosine + spermidine.
-!- PATHWAY: Spermidine biosynthesis; fifth (last) step.
-!- SIMILARITY: Belongs to the spermidine/spermine synthase family.
                MEDLINE-21664373; PubMed=11792842; Shimia K., Yamashita A., Shimiau T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Profeobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
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MEDINE=92041596; PubMed=1938907;
MEDINE=92041596; PubMed=1938907;
MEDINE=92041596; PubMed=1938907;
MUCLectide sequence and expression analysis of the Acetobacter xylinum uridine diphosphoglucose pyrophosphorylase gene.";
J. Bacteriol. 173:7042-7045(1991).
-:- CATALYTIC ACTIVITY: The alpha-D-glucose 1-phosphate = diphosphate + UDF-glucose.
-:- SIMILARITY: Belongs to the prokaryotic UDFGP family.
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Pred. No. 3.18+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 AA; 32992 MW; F546286DA257EB22 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP003187; BAB80256.1; -.
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||::|:
57 DEFIYHDM 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
Type A;
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SEQUENCE

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C. - CATALYTIC ACTIVITY: dTTP + alpha-D-glucose I-phosphate = diphosphate + dTDP-glucose.

C. - CATALYTIC ACTIVITY: dTTP + alpha-D-glucose I-phosphate = CC diphosphate + dTDP-glucose.

C. - PATHWAY: RHAMMOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS CC PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase)
(RFBAI OR NWA0188) AND (RFBA2 OR NWA0205).
                                                                                                                                                                                                                                                                                                                                           ,
                                                                                                                                                                                                                                                                                                Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria; Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 28. 50.0%; Pred. No. 3.2e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                             6C809AFFBBA1791B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; H82014; H82014.

InterPro; IPR005907; GIP_thy_trans_1.

InterPro; IPR005935; NTP_transferase.
Pfam; PF00483; NTP_transferase; 1.

IGRFAMs; TIGR01207; rmlA; 1.

Lipopolysaccharide biosynthesis; Transferase; Kinase;
Nucleotidyltransferase; Complete protecme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                      InterPro; IPR005835; NTP transferase,
Pfam; PF00483; NTP transferase; 1.
Transferase; Kinase; Nucleotidyltransferase.
SEQUENCE 284 AA; 30992 MW; 6C809AFFBBA17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Z2491 / Serogroup A / Serotype 4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL162752; CAB83503.1; -. EMBL; AL162752; CAB83519.1; -.
                                                                                                                                  EMBL; M76548; AAA21888.1; -.
                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae; Neisseria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           :|||::|:
120 REFIGNDP 127
                                                                                                                                                      PIR; A41382; A41382.
                                                                                                                                                                                                                                                                                                                                                                             1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFBA NEIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-MCSB / Serogroup B;

MEDLINE-2017755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair B., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.,

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           2.7.7.24) (dTDP-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:1809-1815(2000).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.
-!- PATHWAY: RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACHARIDE BIOSYNTHESIS.
-!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B1940 / Serogroup B, MEDLINE=94293762; PubMed=8022265; Mamerschmidt S., Birkholz C., Zahringer U., Robertson B.D., van Putten J.P.M., Ebeling O., Frosch M., "Contribution of genes from the capsule gene complex (cps) to liboligesaccharide blosynthesis and serum resistance in Neisseria
                                                                                   0;
                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose-l-phosphate thymidylyltransferase (EC 2.7.7.24) (dTC synthase) (dTDP-glucose pyrophosphorylase).
(RFBA1 OR NMB0062) AND (RFBA2 OR NMB0080).
Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria; Betaproteobacteria, Neisseriales;
                                            Length 288;
                                                                                 Indels
32151 MW; C818727C546F5E00 CRC64;
                                      100.0%; Score 25; DB 1; I
50.0%; Pred. No. 3.2e+02;
ive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR005907; G1P_thy_trans_l.
InterPro; IPR005835; NTP_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L09189; AAC37050.1; ALT INIT.
EMBL; AE002365; AAF40530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 11:885-896(1994).
                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002367; AAF40544.1; -. PIR; B81240; B81240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseriaceae; Neisseria.
NCBI_TaxID=491;
                                                                             4; Conservative
                                                                                                                                          : | | | :: | :
94 EEFIGNDN 101
                                                                                                                    8
288 AA;
                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; NMB0062; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis.";
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RFBA_NEIMB
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1 XEFIXXDX
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ARY2_MOUSE
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                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=UALS) / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Perretti J.J.;
"Genome sequence of Streptococcus mutans UAl59, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase) (dTDP-glucose pyrophosphorvlase)
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate diphosphate + furpP-glucose.
-!- PATHWAY: dTDP-L-rhamnose biosynthesis.
-!- PATHWAY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                 Score 25; DB 1; Length 288; Pred. No. 3.2e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEAIN=XC;
Tsukioka Y., Yamashita Y., Nakano Y., Oho T., Koga T.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5563650C07C00987 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipopolysaccharide biosynthesis; Transferase; Kinase;
Nucleotidyltransferase; Complete proteome.
SEQUENCE 289 AA; 32295 MW; 5563650C07C00987 CRC64
                                                                                                8A65B50B531F2907 CRC64;
 Pfam; PFU0405; with Transferase; Kinase; Lightpopolysaccharide biosynthesis; Transferase; Kinase; Lippopolysaccharide biosynthesis; Transferase; Kinase; Nucleotidyltransferase; Complete proteome.

CONFLICT 125 125 A -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE014978; AAN59119.1; -
InterPro; IPR005907; GIP, thy trans.1.
InterPro; IPR005835; NTP transferase.
Pfam; PP00483; NTP_transferase; 1.
Pfam; PF00483; NTP_transferase; 1.
                                                                                                                                                                         4;
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50.0%; E
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50.0%; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D78182; BAA11247.1;
                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                              94 EEFIGNDN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMLA OR SMU.1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                  RMLA STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                   CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                               RESULT 75
RMLA_STRMU
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Gaps

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4; Conservative

Matches Best

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAL-1 and Nat-2 gene products.";

Mol. Pharmacol. 42:265-272(1992).

-!- FUNCTION: Participates in the detoxification of a plethora of hydrazine and arylamine drugs. 2-aminofluorene and p-aminobenzoic acid (PABA) are preferred substrates for NAT-2. Less activity with anisidine and barely detectable with SMZ.

-!- CATALYTIC ACTIVITY: Acetyl-CoA + an arylamine = CoA + an N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- POLYMORPHISM: There are two forms of NAT2: a rapid/stable isoform (Asn-99) and a slow/unstable isoform (Ile-99).
-!- SIMILARITY: Belongs to the arylamine N-acetyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martell K.J., Levy G.N., Weber W.W.; "Cloned mouse N-acetyltransferases: enzymatic properties of expressed
                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arrylamine N-acetyltransferase 2 (EC 2.3.1.5) (Arrylamide acetylase 2)
(N-acetyltransferase type 2) (NAT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                  Martell K.J., Vatsis K.P., Weber W.W.; "Molecular genetic basis of rapid and slow acetylation in mice."; Mol. Pharmacol. 40:218-227(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=94379961; PubMed=7545952;
Kelly S.L., Sim E.;
"Arylamine N-acetyltransferase in Balb/c mice: identification of novel mouse isoenzyme by cloning and expression in vitro.";
Biochem. J. 302:347-353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C3H/HeJ; TISSUE-Heart;
Hein D.W., Doll M.A.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B61267; B61267.
MGD; MGI:109201; Nat2.
InterPro; IPR004081; AANacetyltransf.
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6, and A/J;
MEDLINE=91342604; PubMed=1875909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92382565; PubMed=1513324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U35886; AAA78943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U35887; AAA78944.1; -. EMBL; U37249; AAA80353.1; -. EMBL; U37250; AAA80354.1; -.
                                                                                                                              STANDARD;
                     :|||::|:
94 EEFIGDDH 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetylarylamine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
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139 TEFIGNDD 146

RESULT 78

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MEDLINE=20031141; PubMed=10566865;

MEDLINE=20031141; PubMed=10566865;

De Lencastre H., Wu S.-W., Pinho M.G., Ludovice A.M., Filipe S., Gardete S., Sobral R., Glil S., Chung M., Tomasz A.;

"Antibiotic resistance as a stress response: complete sequencing of a large number of chromosomal loci in Staphylococcus aureus strain COL that impact on the expression of resistance to methicillin.";

Microb. Drug Resist. 5:163-175(1999).

-!- FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).

-!- SUBUNIT: Monomer (Probable).
                                                                                                                                                                                  Gaps
                                                                                                                                                                                    ·;
                                                                                                                                                       Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; Length 291; 50.0%; Pred. No. 3.2e+02; Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNUCKLE-LIKE CYSTEINE CLUSTER
                                                                                                                                                                                 0; Indels
                                                                                                                          704E000DE48CE557 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D7FE2B5989577D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                 100.0%; Score 25; DB 1;
50.0%; Pred. No. 3.2e+02;
iive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (PROBABLE).
GTP (PROBABLE).
GTP (PROBABLE).
                                                                                                                                                                                                                                                                                                           291 AA.
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4; Mismatches
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                                                                                                            isoform)
                                                                                                                                                                                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Last annotat.
Probable GTPase engC (EC 3.6.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus (strain COL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERM; PF03193; DUF258; 1.
TIGRFAMS; TIGR00157; TIGR00157; 1.
PROSITE; PS50936; ENGC_GTPASE; 1.
Hydrolase; GTP-binding
                                                                                                                       290 AA; 33701 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 258 KM
291 AA; 33890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13639; CAA73981.1; -. HAMAP; MF_01820; -; 1. InterPro; IPR004881; DUF258.
                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
171
218
258
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173 QEFINSDL 180
                                                                                                                                                                                                         1 XEFIXXDX 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        STAAC
                                                                                                                        SEQUENCE
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NP_BIND
                                                                                                                                                                                                                                                                                                      ENGC STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MUSO, ATCC 700699, and N315;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Acki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lancet 339:1819-1827(2002).
-!- FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).
-!- SUBUNIT: Monomer (Probable).
-!- SIMILARITY: Contains 1 engC GTPase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEALN=MW2;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagai Y., Iwama N., Asano K., Nalmı 1., hurowa...,
Yamamoto K., Hiramatsu K.,
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 291;
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                                                                          15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last amoration update)
Probable GTPase engC (EC 3.6.1.-)
ENGC OR SAV1221 OR SA1064 OR MW1104.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain Mu50),
Staphylococcus aureus (strain Mu50),
ENGC OR SAV1000 (STRAIN MU50),
Staphylococcus aureus (strain Mu20).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; PRE LANGE BELLY LANGE B
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Pred. No. 3.2e+02;
                                     291 AA
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003361; BAB57383.1; --
EMBL; AP003133; BAB42316.1; --
EMBL; AP004826; BAB94869.1; --
PIR; H89894; H89894.
HAWAP; MF 01820; --; 1.
InterPro; IPR004881; DUF258.
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                              STANDARD;
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245
291 AA;
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Best Local Similarity
                           STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                              099UP7
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ENGC_STAAM
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1 XEFIXXDX 8

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4; Conservative

Matches

50.08;

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Gaps

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2.7.7.24) (dTDP-glucose

Matches

₹ d RFBA_SALAN

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                                                                                                                                                                                                                                                                                                                      Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R., "Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar typhimurium (strain LT2)."; Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcclelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florara L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphosphate + dTDP-glucose.
PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PROBANTICEN SINGNAMERIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00483; NTP transferase, 1.
TIGREAMS; TIGRO1207; rmlA, 1.
Lipopolysaccharide biosynthesis; Transferase; Kinase;
Nucleotidyltransferase; Complete protecome.
                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-EB-2003 (Rel. 41, Last annotation update)
Succese-1-phosphate thymidylyltransferase (EC synthase)
            292 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro, IPR005907; GIP thy trans_1.
Interpro, IPR005835; NTP_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                            MEDLINE=91260454; PubMed=1710759;
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292 AA; 32453 MW; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                STANDARD;
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StyGene; SG10449; rfbA.
                                                                                                                                                                         Salmonella typhimurium.
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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RFBA SHIFL
ID RFBA SHIFL ST
AC P37779; Q54164;
                                                                                                                                                       STM2095
                                                                                                                                                                                                                                NCBI_TaxID=602
                SALTY
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                RFBA SP
P26393
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STRAIN=M32 / Group E1;
MEDLINE=92201631; PubMed=1372579;
Wang L., Romana L.K., Reeves P.R.;
"Molecular analysis of a Salmonella enterica group E1 rfb gene
cluster: O antigen and the genetic basis of the major polymorphism.";
Genetics 130:429-443 (1992).
                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
Glucose-1.phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=58712;
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Score 25; DB 1; Lengu..
3 No. 3.3e+02; Indels
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipopolysaccharide biosynthesis, Transferase, Kinase, Nucleotidyltransferase.
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4; Mismatches
    Mismatches
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InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase; 1.
TIGRFAMS; TIGR01207; rm18, 1.
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    4;
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Matches 4; Conservative
    Conservative
                                                                                                                                                                               STANDARD;
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                                                                 139 TEFIGNDD 146
                                        1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                       Salmonella anatum
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                                                                                                                                                                               RFBA_SALAN
P55254;
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                                              Gaps
                                             ٠,
                     Length 292;
                                              Indels
11065BA9DF2B0268 CRC64;
                     ; Score 25; DB 1; L. Pred. No. 3.3e+02; 4; Mismatches 0;
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RESULT

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01-OCT-1994 (Rel. 30, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macpherson D.F., Manning P.A., Morona R.; "Characterization of the dTDP-rhamnose biosynthetic genes encoded in the rfb locus of Shigella flexneri."; Mol. Microbiol. 11:281-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of the rhamnose biosynthetic operon of Shigella flexneri 2a and role of lipopolysaccharide in virulence.";
J. Bacteriol. 176:2362-2373(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O ANTIGEN BIOSYNTHESIS
                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIRS_2559074, ATCC 700930 / Serotype 2a;

MEDLINE=2259074; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blather F.R.;

Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-YEH6200 / Serotype 2a;
MEDLINE=94209238; PubMed=8157605;
Rajakumar K., Jost B.H., Sasakawa C., Okada N., Yoshikawa M.,
Adler B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flexheri serotype 2a strain 24577.",
Infect. Immun. 71:2775-2786(2003).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate + dTDD-glucose.
-!- PATHWAY: RHAMNOSE BIOSYNTHESIS WITHIN THE O ANT PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                       s) (dTDP-glucose pyrophosphorylase). SF2102 OR S2225.
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InterPro; IPR005907; G1P thy trans 1.
InterPro; IPR005935; NPF transferase.
Pfam; PF00483; NTP_transferase, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PE577 / Serotype 2a;
MEDLINE=94224146; PubMed=8170390;
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                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X71970; CAA50769.1; -.
EMBL; L14842; AAA53681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Shigella flexneri
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=623;
                                                                                                                                                   synthase)
                                                                                                                                                                                          RFBA OR
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MEDLINE=94292435; PubMed=7517391;
Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
Redmond J.W., Lindquist L., Reeves P.R.;
"Structure of the O antigen of Escherichia coli K-12 and the sequence
                                                                                                                                                                                                                                                                                                                                                                                         2.7.7.24) (dTDP-glucose
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=97486617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The Complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERULNE-K12;
MEDLINE-87251358; PubMed-9097040;
MEDLINE-97251358; PubMed-9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miri T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundarama S., Tagami H., Takeda J., Takemoto K., Wada C., Yanamoto Y., Horiuchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                          0;
100.0%; Score 25; DB 1; Length 292; 50.0%; Pred. No. 3.3e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stevenson G.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           PRT; 293 AA. P37744; P78081; C1-C2-1994 (Rel. 30, Created) C1-CC7-1994 (Rel. 30, Created) C1-CC7-2003 (Rel. 35, Last sequence update) C1-CC7-2003 (Rel. 42, Last annotation update) Glucose-1-phosphate thymidylylcransferase (EC synthase) (GTDP-glucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       its rfb gene cluster.";
Bacteriol. 176:4144-4156(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae, Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [5]
SEQUENCE OF 247-293 FROM N.A.
                                                                                                                                                                                         Conservative
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97 EEFIGGDD 104
                                                                                                                                                                                                                  1 XEFIXXDX 8
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / WG1;
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REVISION TO 288.
STRAIN=K12 / WG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                    RBA1_ECOLI
                                                                                                                                                                                    Matches
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ETT FT
SO FT
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Biochem. 230:906-913(1995)
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Schubert D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SERAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=85324581; PubMed=7601152;
Shima S., Weiss D.S., Thauer R.K.;
Formylmethanofuran:terrahydromethanopterin formyltransferase (Ftr)
from the hyperthermophilic Methanopyrus kandleri. Cloning, sequencing
and functional expression of the ftr gene and one-step purification
of the enzyme overproduced in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
        STRAIN=K12 / W3110;
MEDLINE=94292434; PubMed=7517390;
Yao Z., Valvano M.A.;
"Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) of Escherichia coli K-12 W3110: identification of genes that confer group 6 specificity to Shigella flexneri serotypes Y and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;

    Gacteriol. 176:4133-4143 (1994).
    CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose BIOSYNTHESIS WITHIN THE O ANTIGNED PATHWAY: DTDP-L-RIAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGNED BIOSYNTHESIS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 25; DB 1; Length 293; Pred. No. 3.3e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Libopolysaccharide biosynthesis; Transferase; Kinase; Nuclectidyltransferase; Complete proteone; 3D-structure. CONFLICT 247, Q -> P (IN REF. 5). SEQUENCE 293 Aa; 32693 MW; BA895362DICSCA55 CRC64;
                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EccGene, EG11978; rfbA.
InterPro, IPR005997; G1P thy trans 1.
InterPro, IPR005835; NTP transferase.
Ham, PF00483; NTP transferase; IGRFAMS; TIGR01207; rmlA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000294; AAC75100.1; -.
EMBL; D90841; BAA15881.1; -.
EMBL; U03041; BAA15893.1; -.
EMBL; U03041; AAC31629.1; -.
PIR; F64969; F64969.
PDB; 1H5T; 08-MAY-02.
SWISS-2DPAGE; P37744; COLI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U09876; AAB88400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::|:
97 EEFIGGDD 104
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- FUNCTION: Catalyzes the reversible transfer of a formyl group from formylmethanofuran (formyl-MFR) to tetrahydromethanopterin (H(4)MPT) so as to produce 5-formyl tetrahydromethanopterin (N(5)-formyl-H(4)MPT) and methanofuran (MFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Salt dependence, kinetic properties and catalytic mechanism of N-formylmethanofuran:tetrahydromethanopterin formyltransferase from the extreme thermophile Methanopyrus kandleri.";

Bur. J. Biochem. 210:971-981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanogenesis; One-carbon metabolism; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97341227; PubMed=9195883; Brmler U., Merckel M., Thauer R., Shima S.; "Formylmethanofuran: tetrahydromethanopterin formyltransferase from Methanopyrus kandleri - new insights into salt-dependence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: Methanogenesis from carbon dioxide; second step.
-!- SUBUNIT: Homotetramer composed of two dimers. Dimerization is sufficient for enzyme activity, but tetramerization is required for high thermostability.
SEQUENCE FROM N.A.

STRAIN-AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014;

Slesarev A.I., Mexhevaya K.V., Makarova K.S., Polushin N.N.,

Slcherbinian O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonim B.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A mutation affecting the association equilibrium of formyltransferase from the hyperthermophilic Methanopyrus kandleri and its influence on the enzyme's activity and thermostability."; Eur. J. Biochem. 267:6619-6623(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20507566, PubMed-11054114,
Shima S., Thauer R.K., Ermler U., Durchschlag H., Tziatzios C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetrahydromethanopterin = methanofuran + 5-formyl-5,6,7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tetrahydromethanopterin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breitung J., Borner G., Scholz S., Linder D., Stetter K.O., Thauer R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the FTR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-49, AND CHARACTERIZATION.
MEDLINE=93130924; PubMed=1483480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT, AND MUTAGENESIS OF ARG-261.
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InterPro; IRR002770; FTR.
Pfam; PF01913; FTR, 1.
Pfam; PF02741; FTR C; 1.
PIRSF; PIRSF006414; FTR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE010311; AAM01333.1;
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Structure 5:635-646(1997)
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HAMAP; MF_00579; -; 1
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                         VPO BPHP1
P51719;
                                                                                                                                                               DISŬLFID
DISULFID
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                     VPO_BPHP1
  0
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    R->E: WEAKENS DIMER-DIMER ASSOCIATION.
THERMOLABILE.
H >> D (IN REF. 3).
W -> K (IN REF. 3).
E -> K (IN REF. 3).
                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                  ; Score 25; DB 1; Length 296;
Pred. No. 3.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
33 kDa chaperonin (Heat shock protein 33 homolog) (HSP33).
HSLO OR CAC2370.
Clostridium acetobutylicum.
                                                                                                                                                                                                           31661 MW; DDE02D3E7D98FC86 CRC64;
                                                                                                                                                                                                                                                              297 AA.
 Complete proteome
                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                              STANDARD;
                       :|||::|:
150 GEFIVEDS 157
                                                                                                                                                                                                                                  1 XEFIXXDX 8
                                                                                                                                                                                                          296 AA;
                                                                                                                                                                                                                      Sest Local Similarity
3D-structure;
MUTAGEN 26
                                                                                                                                                                                                                                                     RESULT 84
HSLO_CLOAB
ID HSLO_CLOAB
AC 091636;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

XM MEDLINE=21359325; PubMed=11466286;

XM MEDLINE=21359325; PubMed=11466286;

XM Obson R. J. Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

A Gibson R. L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

R Bennett G.N., Koonin E.V., Smith D.R.;

R Bennett G.N., Koonin E.V., Smith D.R.;

B Bennett G.N., Koonin E.V., Smith D.R.;

A Bennett G.N., Koonin E.V., Smith D.R.;

B Bennett G.N., Koonin E.V., Smith D.R.;

C Bacterium Clostridium acetobutylicum.";

J Bacterium Clostridium and oxidatively damaged proteins from irreversible aggregation. Plays an important role in the bacterial clost in the bacterial conditions conditions are formed converted conditions two disulfide bonds are formed converted conditions woo disulfide bonds are formed converted conditions with the protein is inactive (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Esposito D., Fitzmarrice W.P., Benjamin R.C., Goodman S.D., Waldman A.S., Scocca J.J.,
"The complete nucleotide sequence of bacteriophage HPI DNA.",
Nucleic Acids Res. 24:2360-2386(1996).
-!- SIMILARITY: STRONG, TO PHAGE P2 PROTEIN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PI; Zinc; Complete proteome.
REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
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Pred. No. 3.3e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01430; HSP33; 1.
ProDom; PD248154; Hsp33; 1.
Chaperone; Redox-active center; Zinc; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: Belongs to the HSP33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Probable capsid scaffolding protein (ORF17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 AA; 32033 MW;
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HAMAP; MF 00117; -; 1.
InterPro; IPR000397; Hsp33.
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217 LEFIFEDM 224
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Best Local Similarity
Matches 4; Conserv
                                                                              SEQUENCE FROM N.A.
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Clostridium.
NCBI_TaxID=1488;
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Viruses; dsDNA vi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 298; 50.0%; Pred. No. 3.3e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                               ; Score 25; DB 1; Length 298; Pred. No. 3.3e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein, Complete proteome.
298 AA; 34256 MW; EBD06E78B3D3F8EF CRC64;
                                                                                                                                           298 AA; 33702 MW; 6D2841468D700C1F CRC64;
                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_2144.
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                                                                                  or send an email to license@isb-sib.ch).
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MEDLINE=98196666; PubMed=9537320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                    100.08;
                                                                                                          EMBL; U24159; AAB09202.1; -. PIR; S69523; S69523.
                                                                                                                                                                              50.0%;
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                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                   STANDARD;
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227 EEFILEDF 234
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142 GEFIKVDF 149
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus.
                                                                                                                                 Capsid assembly SEQUENCE 298
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ID Y4IF RHISN
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Bacteria; Firm.cutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                        Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
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                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Pantothenate kinase (BC 2.7.1.33) (Pantothenic acid kinase).
                                                                                                                                                      Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 30 50.0%; Pred. No. 3.48+02; cive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000078; AAB91701.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 305 AA; 34141 MW; 331117881829F351 CRC64;
                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 AA
01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat. Hypothetical 34.1 kDa protein Y41F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                                                                                         Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: None obvious.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:394-401(1997
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113 IEFIRGDI 120
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nes 4; Conserv
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                                                                                                                                                                                                                                         NCBI_TaxID=394;
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SEQUENCE 30
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us-09-660-302e-1.rsp

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                                or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91139580; PubMed=1899858;
                                                        EMBL; AL766848; CAD46598.1; -.
EMBL; AE014235; AAM99835.1; -.
SagaList; gbs0939; -.
TIGR; SAG0951; -.
                                                                                                                                                                                                                                                          36093 MW;
                                                                                                                                                                                                                                                                                           100.08;
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NP_BIND 91
SEQUENCE 306 AA;
                                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
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STRAIN=2603 V/R / Scrotype V;
STRAIN=2203 V/R / Scrotype V;
STRAIN=22222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu K., Lewis M.R., Radure D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carry H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Riccobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Ringudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphopantothenate.
-!- PATHWAY: Coenzyme A (COA) biosynthesis; first step.
-!- SUBCELDULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of an
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                                                                                                                                                                                      Score 25; DB 1; Lengu...
No. 3.4e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          QBESPZ; QBDZZI;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pantothenate Kinase (EC 2.7.1.33) (Pantothenic acid Kinase).
                                                                                                                                                                                                                       Length 306;
                                                                                            Pfam; PF00485; PRK; 1.
PIRSF: PIRSF000545; Pantothenate kin; 1.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agaiactiae (serotype v).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                   ATP (POTENTIAL).
: 87241BDFC3FC9DB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus agalactiae (serotype III), and Streptococcus agalactiae (serotype V).
                                                                                                                                                                                                                                 Pred. No. 3.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
             EMBL; AE006374; AAK05542.1; -. PIR; D86805; D86805, D86805. 1. HAMAP; MF_00215; -; 1. InterPro; IPR004566; Pank bact. InterPro; IPR006083; PRK_URK.
                                                                                                                                                                               SEQUENCE 306 AA; 35992 MW;
                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                 50.0%;
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NEFINFDE 9
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Bronillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.G., Connerton I.F., Cummings N.G., Daniel R.A.,
Brian K.D., Errington J., Rabret C., Ferrari B., Foulger D.,
Rritz C., Fujita M., Fujita Y., Fabret C., Rerrari B., Foulger D.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.G., Grandi G.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kutita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=29194547; PubMed=1901616;
Perego M., Higgins C.F., Pearce S.R., Gallagher M.P., Hoch J.A.;
The oligopeptide transport system of Bacillus subtilis plays a role in the intriation of sporulation.";
Mol. Microbiol. 5:173-185(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rudner D.Z., Ledeaux J.R., Ireton K., Grossman A.D., "The spook locus of Bacillus subtilis is homologous to the oligopeptide permease locus and is required for sporulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 306;
HAMAP; MF 00215; -; 1.
InterPro; IPR04566; Pank bact.
InterPro; IPR066083; PRK ÜRK.
Pro; PF00485; PRK; I.
PIRSF; PIRSF000545; Pantothenate kin; 1.
Transferase; Khnase; ATP-binding; Coenzyme A biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
. 01FF015134D76D34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 1; Le
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPPF BACSU STANDARD; PRT; 308 AA. P24137; O31599; P23366; 01-MAR-1992 (Rel. 21, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Oligopeptide transport ATP-binding protein oppF. OPPF OR SPOOKE OR BSU11470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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us-09-660-302e-1.rsp

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SECUENCE FROM N.A.
                                                                                                                                                                   SEQUENCE OF 1-35.
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Park Darvo V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagashi H., Tackemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tarkmaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tarepstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandelor M., Vannier F., Vassarotti A.,
Vari A., Wambutt R., Wedler E., Medler T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
T. "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.
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                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).

-i- FUNCTION: Component of the oligopeptide permease, a binding protein-dependent transport system. Necessary for genetic protein-dependent transport system. Probably responsible for energy competence but not sporulation. Probably responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Competence; Peptide transport; Transport; Membrane; ATP-binding;
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Pred. No. 3.5e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  coupling to the transport system.
SUBCELLUIAR LOCATION: Membrane-associated.
SIMILARITY: Belongs to the ABC transporter family.
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EMBL; M57689; AAA62692.1; -.
EMBL; M57689; AAA62693.1; ALT_INIT.
EMBL; Z99110; CAB33004.1; ALT_INIT.
PIR; E38447; E38447.
Subtilist; BG10775; oppr.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003493; AAC_transporter.
Pfam; PF00005; ABC_transporter.
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ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
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01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last anno
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PEFIIADE 179
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Matches 4; Conserv
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NCBI_TaxID=1108;
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A interpro; IRROUGLO.,
A interpro; IRROUGLO.,
B Pfam; PF00866; Idh, 1.
B Pram; PF02866; Idh C; 1.
DR PRINTS; PR00066; LiDHDRGRASE.
DR PROSTE; PS00066; MDH; FALSE NEG.
DRACT SITE 148
B SINILARITY).
FT ACT SITE 148
B SINILARITY).
FT SITE 151
B SUBSTRATE CARROYL (BY SIMILARITY).
FT SITE 175
B PROTON-RELAY (BY SIMILARITY).
FT SITE 175
FT SINILARITY).
FROTON-RELAY (BY SIMILARITY).
FT SITE 175
FORDON-RELAY (BY SIMILARITY).
FT SITE 175
FORDON-RELAY (BY SIMILARITY).
FROTON-RELAY (BY SIMILARITY).
FT SITE 175
FORDON-RELAY (BY SIMILARITY).
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F
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Malate dehydrogenase from the thermophilic green bacterium chloroflexus aurantiacus: purification, molecular weight, amino acid composition, and partial amino acid sequence.";

J. Bacteriol. 170:2947-2953(1988).

-!-CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.

-!-SUBUNIT: HOMOTETRAMER (ACTIVE BNZYME); HOMODIMER AND HOMOTRIMER.

AT TEMPERATURES LOWER THAN 55 DEGREES CELSIUS (INACTIVE FORMS).

-!-SIMILARITY: Belongs to the LDH family. MDH subfamily.
STRAIN=J-10-f1;
MEDLINE=96241868; PubMed=8661927;
Synstad B., Emmerhoff O., Sirevag R.;
"Malate dehydrogenase from the green gliding bacterium Chloroflexus aurantiacus is phylogenetically related to lactic dehydrogenases.";
Arch. Microbiol. 165:346-353 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92250599; PubMed=1339458;
Schlaepfer D.D., Fisher D.A., Brandt M.E., Bode H.R., Jones J.M.,
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Hydridae; Hydra.
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Pred. No. 3.5e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 22, Last sequence update)
Annexin B12 (Annexin XII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=J-10-f1;
MEDLINE=88257004; PubMed=3133356;
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PDB; 1GUY; 13-JUN-02.
INTERPO; IPRO01557; L.DH.
INTERPO; IPRO01236; JÄh.
INTERPO; IPRO01252; MÄH. AS.
INTERPO; IPRO02057; NAD_BS.
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                                                                                                               X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF MUTANT LYS-105.
MEDLINE=20170873; Pubmed=10704197;
Cartailler J.P., Haigler H.T., Luecke H.;
Annexin XII E105K Crystal structure: identification of a pH-dependent switch for mutant hexamerization.";
Biochemistry 39:2475-2483(2000).
-- SUBBUIT: Homohexamer.
                                                                                                                                                                                      DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

PHY: Phosphorylated in vitro on serine(s) and threonine(s) by PKC. SIMILARITY: Belongs to the annexin family.

SIMILARITY: Contains 4 annexin repeats.

DATABASE: NAME-Annexin 12 home page from Luecke's group;

WWW="http://anx12.bio.uci.edu/~hudel/anx12/".
Characterization, cDNA cloning, and protein kinase C phosphorylation
                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=96085034; PubMed=7477411;
Luecke H., Chang B.T., Maillard W.S., Schlaepfer D.D., Haigler H.T.;
"Crystal structure of the annexin XII hexamer and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANNEXIN 4.
PHOSPHORYLATION (BY PKC) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 3.
Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
             annexin XII.";
Biol. Chem. 267:9529-9539(1992).
                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1AEI; 20-AUG-97.
PDB; 1DM5; 20-MAR-00.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                             EMBL; M83736; AAA29206.1; -. PIR; A42660; LUJF12.
                                                                                            Nature 378:512-515(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {RNA}(N).

--- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, beta, 1 beta' and 1 omega subunit (By similarity).

--- DOMAIN: The N-terminal domain is essential for RNAP assembly and basal transcription, whereas the C-terminal domain is involved in interaction with transcriptional regulators and with upstream promoter elements (By similarity).

--- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase alpha chain (BC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA N-TERMINAL DOMAIN (ALPHA-NTD)
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ALPHA C-TERMINAL DOMAIN (ALPHA-CTD)
                                                                                                                                     0;
                                                                                          100.0%; Score 25; DB 1; Length 316; 50.0%; Pred. No. 3.6e+02; Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00662; RPOLD; 1. _ _ _ Transferase; Transferase; Transcription; DNA-directed RNA polymerase;
                                                        35108 MW; 10599869CBA853EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q9KWU6; 1HQM.

HAMMP; MF 00059; -; 1

InterPro; IPR009025; RBP11-like RNApo.
InterPro; IPR001700; RNA polA bac_org.
Pfam; PF01000; RNA pol A bac; 1.
Pfam; PF03118; RNA pol A cTD; 1.
ProDom; PR03118; RNA pol A cTD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
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30-MAY-2000 (Rel. 39, Last seque
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392:353-358(1998).
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
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301
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316 AA;
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Aquifex aeolicus.
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254 GEFIKIDQ 261
                 1 XEFIXXDX 8
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Translocates protons across the thylakoid membrane and
transfers electrons from photosystem II to photosystem I. It
receives electrons from the Rieske iron-sulfur protein and passes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COVALENT) (BY SIMILARITY).
(COVALENT) (BY SIMILARITY).
(HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                                                                                       Gaps
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Wakasugi T., Nishikawa A., Yamada K., Sugiura M.;
"Complete nucleotide sequence of the chloroplast genome from a fern,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein (By similarity).
--- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-anchored (By similarity).
--- SIMILARITY: Belongs to the cytochrome c family.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
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InterPro; IPR002325; ADOCYL F.

InterPro; IPR000345; CytC heme BS.

Pfam, PF01333; Apocytochr F C; 1.

PRNTNS; PR00610; CYTOCHROME F.

PROSITIE; PS00190; CYTOCHROME C; 1.

Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
IRON (HEME AXIAL LIGAND) (VIA AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
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                                                                         Score 25; DB 1; Length 317;
Pred. No. 3.6e+02;
; Mismatches 0; Indels
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                       317 AA; 35768 MW; BC6EEB9015163335 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
(BY SIMILARITY)
                                                                                                         Pred. No. 3.6e
4; Mismatches
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50.0%;
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SEQUENCE FROM N.A.
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MEDLINE=87218454; PubMed=3034567;
Luedin C., Hofstetter H., Sarfati M., Levy C.A., Suter U., Alaimo D.,
Kilchherr E., Frost H., Delespesse G.;
"Cloning and expression of the cDNA coding for a human lymphocyte IgE
                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Low affinity immunoglobulin epsilon FC receptor (Lymphocyte IgE
receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94191542; PubMed=8142907; Padlan B.A., Helm B.A.; Helm B.A.; "Modeling of the lectin-homology domains of the human and murine low-affinity Fc epsilon receptor (Fc epsilon RII/CD23).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87051737; PubMed=2877743;
Kikutani H., Inui S., Sato R., Barsumian E.L., Owaki H.,
Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T.,
Tsunasawa S., Sakiyama F., Suemura M., Kishimoto T.;
"Molecular structure of human lymphocyte receptor for immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yokota A., Kikutani H., Tanaka T., Sato R., Barsumian E.L., Suemura M., Kishimoto T., "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23): tissue-specific and IL-4-specific regulation of gene expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=93038513; PubMed=1417742;
MEDLINE=93038513; Turactif G., Graber P., Pochon S., Regamey P.-O.,
Jansen K.U., Magnenat E., Aubonney N., Bonnefoy J.-Y.;
"Partial characterization of natural and recombinant human soluble
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human lymphocyte Fc receptor for 1gE: sequence homology of its cloned cDNA with animal lectins.";
Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-87118255; PubMed=2949326;
Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,
   321 AA.
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3D-STRUCTURE MODELING OF LECTIN DOMAIN.
PRT;
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MEDLINE=96276216; PubMed=8745401;
Bajorath J., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. J. 286:819-824(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.";
EMBO J. 6:109-114(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor 3:325-341 (1993)
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 47:657-665(1986).
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        Nature 374:193-196(1995)
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                                                                                                                                                                                321 AA;
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Best Local Similarity
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STRAIN=S288C;
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SEQUENCE FROM N.A.
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                                                                                                                                             PTM: N- and O-glycosylated.

MISCELLANEOUS: There are two kinds of Fc receptors for 1gE, which differ in both structure and function: high affinity receptors on basophils and mast cells and low affinity receptors on lymphocytes
"Structure-based modeling of the ligand binding domain of the human cell surface receptor CD23 and comparison of two independently derived molecular models.";

Protein Sci. 5:240-247(1996).

-!- FUNCTION: This receptor has essential roles in the regulation of IgE production and in the differentiation of B-cells (it is a B-cell-specific antigen).

-!- SUBCELMULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A SOLUBLE EXCRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
MEEGQYS -> MNPPSQ (in isoform B).
//TTGVSP 003057.
//TTGVSP 003057.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Prints, Profess, lectin c; 1.

PRINTS; PR00356; ANTIFREEZEII.

PROSITE; PR0034; CLECT; 1.

PROSITE; PS50041; C_TYPE_LECTIN 1; 1.

PROSITE; PS50041; C_TYPE_LECTIN 2; 1.

Receptor; Antigen; TgE-bInding Protein; Repeat; Signal-anchor; Transmembrane; Lectin; Glycoprotein; Alternative splicing;
                                                                                                                                                                                           SIMILARITY: Contains 1 C-type lectin family domain. DATABASE: NAME=PROW, NOTE=CD guide CD23 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL) . (LONG FORM)
                                                                                                                                                                                                                                                                                                           EMBL; M15059; AAA52434.1; --
EMBL; M14766; AAA52435.1; --
EMBL; M20472; CAA28465.1; --
EMBL; M20562; AAA52433.1; --
EMBL; M2067; LNHUER.
PDB; 1HLI; 31-7AN-94.
PDB; 1KJB; 03-APR-96.
Genew; HGNC:3612; FCER2.
MM; 151445; --
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005178; F:integrin binding; TAS.
InterPro; IPR002353; Antifreezeil.
                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (C-TYPE LECTIN (CLEAVAGE.
                                                                                                                                     IsoId=P06734-2; Sequence=VSP_003057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
SIMILARITY.
                                                                                                        Name=A;
Isold=P06734-1; Sequence=Displayed;
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VARSPLIC
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REPEAT
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Gaps
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: UME5/SRB10 and UME3/SRB11 form a kinase-cyclin pair in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuchin S., Yeghlayan P., Carlson M.;
"Cyclin-dependent protein kinase and cyclin homologs SSN3 and SSN8
contribute to transcriptional control in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 92:4006-4010(1995).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FB-2004 (Rel. 43, Last annotation update)
FNMAR.2004 (Rel. 43, Last annotation update)
FNA polymerase II holoenzyme cyclin-like subunit.
UME3 OR SSN8 OR SFB11 OR YNLO25C OR N2805.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao S.-M., Zhang J., Jeffrey D.A., Koleske A.J., Thompson C.M., Chao D.M., Viljoen M., van Vuuren H.J.J., Young R.A.;
"A kinase-cyclin pair in the RNA polymerase II holoenzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert
                                                                                                                                              ·,
                                                                          Length 321;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith J.B., Mallory M.J., Strich R.;
Submitted (XXX-1995) to the EMBL/GenBank/DDBJ databases.
36468 MW; F86708C0E6515B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                Score 25; DB 1; L
Pred. No. 3.6e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA
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MEDLINE=95249601; PubMed=7732022;
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-!- COFACTOR:
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RIR2_ASFM2
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MDDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Mokenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., Mokenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback F.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
the RNA polymerase II holoenzyme, and are essential for a normal transcriptional response to galactose induction in vivo, and are involved in CTD (carboxy-terminal domain) phosphorylation and this modification has a role in the response to transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Nature 390:364-370(1997).
                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: Belongs to the cyclin family. Cyclin C subfamily.
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Pred. No. 3.6e+02;
4; Mismatches 0; Indels
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InterPro; IRPR006670; Cyclin.
InterPro; IPR006671; Cyclin.N.
PF00134; Cyclin, 1.
SWART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
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(Rel. 40, Last seq
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                        EMBL; U20221; AAA69820.1; -.
EMBL; U16248; AAA64270.1; -.
EMBL; U20655; AAA85744.1; -.
EMBL; Z71301; CAA5887.1; -.
PIR; S59373; S59373.
GermOnline; 143032; -.
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nes 4; Conservative
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                                                                                                   regulators in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 PEFIPPDP 157
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028970;
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-!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized
thioredoxin + H(2)O = ribonucleoside diphosphate + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps

    -!- PATHWAY: DNA replication pathway; first step.
    -!- SUBUNIT: Heterodimer of a large and a small chain.
    -!- SIMILARITY: Belongs to the ribonucleoside diphosphate reductase

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P29095, LAIS.

TIGR, AF1299; -.
HAMAP, MF 00383; -.
InterPro; IPR0006670; Cyclin.
InterPro; IPR000812; TFIIB euk.
Pfam; PF00382; transcript Fac2; 2.
PRINTS, PR00085; TFACTORIB.
PRINTS; R00385; CYCLIN.
PROSITE; PS00782; TFIIB; 2.
Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
FUNCTION: Stabilizes TBP binding to an archaeal box-A promoter. Also responsible for recruiting RNA polymerase II to the preinitiation complex (DNA-TBP-FIIB) (By similarity).

COFACTOR: Binds 1 zinc ion per subunit (By similarity).

SIMILARITY: Belongs to the TFIIB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

**BEDINES-91335775; PubMed=1871976; Burshell B., Dixon L.,

Bourshell M., Shaw K., Yanez R.J., Vinuela E., Dixon L.,

"The sequences of the ribonucleotide reductase genes from African swine fever virus show considerable homology with those of the orthopoxyirus, vaccinia virus.";

Virology 184:411-416(1991).
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonucleoside-diphosphate reductase small chain (BC 1.17.4.1)
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Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
NCBI_TaxID=10500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thioredoxin.
COFACTOR: Binds 2 iron ions per subunit (By similarity).
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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Pred. No. 3.7e+02;
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AECO1014; AAB89947.1; -. PIR; B69412; B69412.
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3226
328
330
493
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45 GEFICODC 52
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small chain family

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01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CDP-6-deoxy-L-threo-D-glycerc-4-hexulose-3-dehydrase reductase (CDP-6-deoxy-delta-3, 4-glucoseen reductase) (EC 1.17.1.-) (E3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Y peetis; STRAIN=CO-92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; Minch B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quall M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pseudotuberculosis,
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 1; Length 327; Pred. No. 3.7e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E78508DB1978F4B0 CRC64;
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SPECIES=Y.pestis; STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AA.
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4; Mismatches
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                                                                                                                                                                                                                                                                                                         EMBL; M64728; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38966 MW;
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50.0%; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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191 NEFISRDE 198
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Best Local Similarity
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                                                                                       LO S.F., Miller V.P., Lei Y., Thorson J.S., Liu H.-W., Schottel J.L., "CDP-6-deoxy-delta 3,4-glucoseen reductase from Yersinia pseudotuberculosis: enzyme purification and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: PARTICIPATES IN THE CONVERSION OF CDP-6-DEOXY-D-GLYCERO-L-THREO-4-HEXULOSE TO 3,6-DIDEOXY-D-GLYCERO-D-GLYCERO-4-HEXULOSE TO 3,6-DEOXY-D-GLYCERO-L-THREO-4-HEXULOSE-3-DEHYDRASE (E1) IN TWO CONSECUTIVE STEPS. THE DETAILED MECHANISM OF E3 IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                      Thorson J.S., Lo S.F., Ploux O., He X., Liu H.-W.;
"Studies of the biosynthesis of 3,6-dideoxyhexoses: molecular cloning
and characterization of the asc (ascarylose) region from Yersinia
pseudotuberculosis serogroup VA.";
J. Bacteriol. 176:5483-5493(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: In the N-terminal section; belongs to the 2Fe2S plant-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- PATHWAY: Biosynthesis of CDP-ascarylose, a dideoxyhexose from the cell wall lipopolysaccharide.
-:- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Y.pseudotuberculosis,
MEDLINE=97121283; PubMed=8961949;
Johnson D.A., Gassner G.T., Bandarian V., Ruzicka F.J., Ballou D.P.,
Reed G.H., Liu H.-W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Kinetic characterization of an organic radical in the ascarylose biosynthetic pathway."; Biochemistry 35:15846-15856(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=Y.pseudocuberculosis;
MEDLINE=9664885; PubMed=8672475;
Gassner GT., Johnson D.A., Liu H.-W., Ballou D.P.;
"Kinetics of the reductive half-reaction of the iron-sulfur
flavoenzyme CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase
                                                                                                                                                                                                                                                             Kessler A.C., Haase A., Reeves P.R., "Molecular analysis of the 3,6-dideoxyhexose pathway genes of
                                                                                                                                                                                                                            SPECIES=Y.pseudotuberculosis; STRAIN=M85 / Serotype IIA;
MEDLINE=93186709; Pubmed=8444803;
                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Y.pseudotuberculosis, STRAIN-Serotype VA;
MEDLINE=94350832; PubMed=8071227;
                                                                                                                                                                                                                                                                                                         Yersinia pseudotuberculosis serogroup IIA.";
J. Bacteriol. 175:1412-1422(1993).
                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. SPECIES=Y.pseudotuberculosis; STRAIN=V; MEDLINE=94117382; PubMed=8288541;
 Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                      Bacteriol, 176:460-468(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ414155; CAC92352.1; -. EMBL; AE013710; AAM84648.1; -.
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AF461770; AAB49398.1; --
L33181; AAA88698.1; --
S72887; AAB31754.1; --
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PIR; A36952; A36952.
PIR; AE0378; AE0378.
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                      cloned gene.";
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EMBL;
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J. Bacteriol. 179:71357156 (1997).

methylpentanoate (3-isopropylmalate) to 3-carboxy-2-hydroxy-4-methyl-2-methylpentanoate (3-isopropylmalate).
                                                                                                                             Pfam; PF00111; fer2; 1. ——
Pfam; PF00175; NAD binding_1; 1.
PRINTS; PR00371, FFDVCR.
PRINTS; PR00410; PFBLYDRIASE.
PROSTIE; PS00197; 2FE2S FERREDOXIN; 1.
Oxidoreductase; Electron transport; Metal-binding; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                          (BY SIMILARITY).
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
-!- PATHWAY: Leucine biosynthesis; third step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxopentanoate. The product decarboxylates to 4-methyl-2
                                                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 1; Length 328; Pred. No. 3.7e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           8D03600925CB4012 CRC64;
                                                                                                                                                                                                                                                                           IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FBB-2003 (Rel. 39, Last sequence update) 3-isopropylmalate dehydrogenase (BC 1.1.1.85) (IMDH) (3.1Pm.DH).
                                                                                                                                                                                                                                                              FERREDOXIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AA.
                                            InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FPN CYL redCtse.
InterPro; IPR001433; Oxred FDD/NAD(P)
InterPro; IPR001221; Phe hydroxylase.
PEam; PF00970; FAD_binding_6; 1.
             2Fe2S fd BS.
FAD binding_6.
Ferredoxin.
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                                                                                                                                                                                                                             proteome.
                                                                                                                                                                                                                                                                                                                                             35915 MW;
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INIT MET 0 0
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               InterPro; IPR006058;
                              InterPro; IPR008333;
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30-MAY-2000 (
30-MAY-2000 (
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Pfam; PF00180; isodh; 1.
PR0SITE; PS00470; IDH IMDH; 1.
Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
SEQUENCE 329 AA; 35785 MW; E56803788013E5CF CRC64;
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Best Local Similarity
Local 4; Conserve
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1 XEFIXXDX 8 Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 300 summaries

sp plan: *
sp rodent: *
sp virus: *
sp vertebrate: *
sp_unclassified: * sp archea:*
sp bacteria:*
sp fungi:*
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sp human:*
sp nvertebrate:*
sp mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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123 16 Q8YEY2 123 16 Q8EH18	124 2	127 9	129 12	130 10	130 11	130 12	131 16	132 13	132 13	133 5	135 16	136 16	137 16	137 16	140 2	140 2	140	141 4	141 4	142 10	144 12	144 12	145 16	145 16	146 12	147 9	148 5	148 5	149 16	151 16	154 b	154 2	155 16	156 9	156	157 4	157 1	158	160 5	160 1	160	161 2	161 9	163 1	163 1	164 2	164 5	164 1	164 1
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Mon Sep 13 10:53:34 2004

ALIGNMENTS

32 AA

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Gaps

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Conservative

1 XEFIXXDX

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092907 rickettsia

08pc6z xanthomonas

08pc6z xanthomonas

07wmd3 bordetella

07ws6 bordetella

07vz56 bordetella

07vx56 bordetella

07vz56 mycobacteri

08s555 mycobacteri

08s553 arabidopsis
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                       092gw7 rickettsia
088b25 pseudomonas
087a23 xylella fas
090fx1 homo sapien
09pa77 xylella fas
09zwd5 rhizobium m
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O9at50 fucus vesic
O93p81 microscilla
O7v0t3 prochloroco
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001594 caenorhabdi
039127 arabidopsis
08eng2 oceanobacil
0980f1 sulfolobus
081m90 bacillus an
07w994 bordetella
07vyg1 bordetella
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081p71 bacillus an
          Q8y2e2 ralstonia s
Q98m47 rhizobium l
  agrobacteri
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Q81s18 bacillus an
O29541 archaeoglob
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28gjc7 campylobact
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Q9AT50
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Q818V5
Q97KD2
Q7VCY6
Q8GJC7
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Q7WMD3
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Q914X9
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Q98HV7
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=96285745; PubMed=8725005;

MEDLINE=96285745; PubMed=8725005;

Becker J., Brandel M.;

"Molecular cloning and characterization of the pyrB gene of

"Molecular eloning and characterization of the pyrB gene of

Eactobacillus letchmannii encoding aspartate transcarbamylase.";

Biochimie 78:3-31(1996).

EMBL; X84262; CAA59022.1; -.

InterPro; IPR005847; Pept_M38_regn.

Probom; P0000518; Urease; 1.

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Stein S., Liehr T., Eschrich K.;
"Characterization of the mouse liver fructose-1,6-bisphosphatase
                                                                                                                                                                                                                                                                                                                                                                                         ..
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900; GO:0042132; F:functose-bisphosphatase activity; IEA.

90; GO:0016787; F:hydrolase activity; IEA.

90; GO:0042578; F:phosphoric ester hydrolase activity; IEA.

90; GO:005975; P:prosphoric ester hydrolase activity; IEA.

1nterPro: IPR00016; In FB_phphtase.

PF00316; PBPases; II.
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                         Dihydro-orotase (Fragment).
Lactobacillus leichmannii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
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SEQÜENCE 32 AA; 3505 MW; 85797BB62D33540E CRC64;
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4513 MW; 4B5CE6D9E980B0FB CRC64;
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EMBL; AJ245389; CAB65268.1; -.
HSSP; P00636; ICNQ.
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           01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2003 (TrEMBLrel. 25,
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TISSUE=Liver;
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39 AA;
                                                                                                                       NCBI_TaxID=28039;
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Q9QXC5

RESULT 3 Q9QXC5

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MEDLINE=21113149; PubMed=11160885; Chopin A., Sorokin A., Bhrlich S.D., Chopin M.-C.; Chopin A., Bolotin A., Sorokin A., Bhrlich S.D., Chopin M.-C.; Manalysis of six prophages in Lactococcus lactis IL1403: different generic structure of temperate and virulent phage populations."; Nucleic Acids Res. 29:644-651(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF5.
Bacteriophage bIL311.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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EMBL, AF323672; AAK08437.1; -.
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woisofnik M., Podbielski A.;
submitted (PEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U35377; AAF08588.1; -.
HSSP, P03005; LJWE.
GO, GO:0005524; FATP binding; IEA.
GO, GO:0005549; F:ATP binding; IEA.
GO, GO:000560; P:DNA helicase activity; IEA.
GO, GO:0006260; P:DNA replication; IEA.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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54 54
54 AA; 6222 MW; E053B5D20762B9DA CRC64;
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Pfam; PF00772; DnaB; 1.
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                   XEFIXXDX 8
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Bacteria; Spirrchaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
MEDILINE=21147931; PubMed=11250076;
Stein S., Liehr T., Eschrich K.;
"Characterization of the mouse liver fructose-1,6-bisphosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 264:215-224(2001).

L Gene 264:215-224(2001).

R EMBL; AJ242919; CAB65255.1; -.

R MGD; MGI:95492; Fbpl.

N MGD; MGI:95492; Fbpl.

N MGO; MGI:95492; Fiructose-bisphosphatase activity; IEA.

R GO; GO:0042578; F:phosphoric ester hydrolase activity; IEA.

DR GO; GO:005975; P:carbohydrate metabolism; IEA.

DR GO; GO:005975; P:carbohydrate metabolism; IEA.

InterPro; IPR000146; In FB_phphtase.
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AE011618; AANS1883.1;
Hypothetical protein; Complete proteome.
SEQUENCE 50 AA; 6252 MW; 871A05BF16474779 CRC64;
                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fructose-1.6-bisphosphatase (EC 3.1.3.11) (Fragment).
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GEFIMVDR 10
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Plasmid 19:46-56(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94358883; PubMed=8078071;
Janosi L., Yonemitsu H., Hong H., Kaji A.;
"Molecular cloning and expression of a novel hydroxymethylcytosine-
specific restriction enzyme (PvuRtsII) modulated by glucosylation of
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murata T., Ohnishi M., Ara T., Kaneko J., Han C.-G., Li Y.F., Takashima K., Nojima H., Nakayama K., Kaji A., Kamio Y., Miki T., Morti H., Ohtsubo E., Terawaki Y., Hayashi T.; "Complete Nucleotide Sequence of Plasmid Rts1: Implications for Bvolution of Large Plasmid Genomes.";
J. Bacteriol. 184:3194-3202(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mochida S., Tsuchiya H., Mori K., Kaji A.;
"Three short fragments of Rtsl DNA are responsible for the
temperature-sensitive growth phenotype (tsg) of host bacteria.";
J. Bacteriol. 173:2600-2607(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tian Q.B., Ohnishi M., Tabuchi A., Terawaki Y.,
"A new plasmid-encoded proteic killer gene system: cloning, sequencing, and analyzing hig locus of plasmid Rtsl.",
Biochem. Biophys. Res. Commun. 220:280-284(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murata T., Hayashi T.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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MEDLINE=88139175; PubMed=3277947;
Tanaka M., Okawa N., Mori K., Suyama Y., Kaji A.;
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MEDLINE=22024716; PubMed=12029035;
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MEDLINE=88289863; PubMed=2840681;
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22,
24,
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ORF90.
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        1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                     Proteus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=585;
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Nucleotide sequence of an Rts1 fragment causing temperature-dependent
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Terawaki Y., Kakizawa Y., Takayasu H., Yoshikawa M.;
Terawaki Y., Kakizawa Y., Takayasu H., Yoshikawa M.;
Temperature sensitivity of cell growth in Escherichia coli associated
with the temperature sensitive R(KM) factor.";
Nature 219:284-285(1968).
EMBL; AP004237; BAB93653.1;
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                      Mollet B., Clerget M., Meyer J., Iida S.,
"Organization of the Tn6-related kanamycin resistance transposon
Tn2660 carrying two copies of IS26 and an IS903 variant, IS903. B.";
J. Bacteriol. 163:55-60 (1985).
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"Nucleotide sequence of an incompatibility region of mini-Rts1 that
contains five direct repeats.";
J. Bacteriol. 155:1185-1191(1983).
                                                                                                                                                                                                                                                                                                                                          MEDLINE=84185439; PubMed=6325393;
Ramio Y., Tabuchi A., Itch Y., Katagiri H., Terawaki Y.;
"Complete nuclectide sequence of mini-Rts1 and its copy mutant.";
J. Bacteriol. 158:307-312(1984).
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Burkholderiaceae; Ralstonia.
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100.0%; Score 25; DB 2; Lengtu ...
Pred. No. 5.4e+02;
0; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                      instability.";
J. Bacteriol. 170:1175-1182(1988).
                                                                                                                                        MEDLINE=85234397; PubMed=2989253;
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MEDLINE=21681879; PubMed=11823852;
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01-JAN-1998 (TrEMBLrel. 05,
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Matches 4; Conservative
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40 SEFISEDP 47
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40 SEFISFDP 47
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SECOLORICE FROM N.A.
STRAIN=22491, Netrogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quall M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitchead S., Spratt B.G., Barrell B.G.; train of Neisseria
meningitidis 22491."
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI_TaxID=65699;
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                                                                                 100.0%; Score 25; DB 16; Length 65; 50.0%; Pred. No. 6.2e+02; tive 4; Mismatches 0; Indels
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Fraser D.G., Bailey E.;
"Extensive Polymorphism at the Horse DQA Locus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF115325; AAD19975.1;
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EMBL; AL162754; CAB84063.1; -.
PIR; E81922; E81922.

Hypchetical protein; Complete proteome.

SEQUENCE 67 AA; 8031 MW; 34350E84C0AD0DB8 CRC64;
                      Hypothetical protein, Complete proteome. SEQUENCE 65 AA; 7398 MW; C63E96C2631ED973 CRC64;
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01-MRY-1999 (TrEMBLrel. 10, Created)
01-MRY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II DQ-alpha (Fragment).
                                                                                                                                                                                                                                                                                                                                                       Q9JVM2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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  EMBL; AL646074; CAD16977.1;
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16 YEFIFPDQ 23
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EEFIRSDV 42
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Best Local Similarity
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                                                                                        Query Match
Best Local Similarity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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STRANTH-ATTC 824 / DSM 792 / VKM B-1787;
MEDILINE-185925; Pubmed-11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
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                                                                                                                                                                                                      100.0%; Score 25; DB 7; Length 68; S0.0%; Pred. No. 6.5e+02; tive 4; Mismatches 0; Indels
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"Polymorphism and multiple loci for the horse DQA gene.";
Immunogenetics 47:487-490(1998).
EMBL; U92514; AAC17578.1; -.
EMBL; U92514; AAC17578.1; -.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001003; MHC II alpha.
Pfam; PF00993; MHC II alpha; 1.
NON TER
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SEQÜENCE 68 AA; 7992 MW; 8A522AF80CC51581 CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
CACO003.
                                                                                                                                                  68 AA; 8004 MW; 8A522AE225C51581 CRC64;
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01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II DQ-alpha (Fragment).
ELA-DQA.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001003; MHC_II_alpha.
Pfam; PF00993; MHC_II_alpha; 1.
NON_TER 1 68 68
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us-09-660-302e-1.rspt

Matches

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RESULT 13

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TEXAMINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TRAINING OF THE PROPERTY OF THE PROPERTY OF TRAINING OF THE OFFICE O
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                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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SEQUENCE 71 AA; 8334 MW; B2551547303A57AB CRC64;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim S., Komano T.,
"Nucleotide sequence of the R721 shufflon.",
J. Bacteriol. 174:7053-7058 (1992).
GO; GO:0046821; C:extrachromosomal DNA, IEA.
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MEDLINE=93015772; PubMed=1400257;
                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K-12; TRANSPOSON=Tn7;
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PROSITE; PS50889; S4; 1.
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57 DEFIENDF 64
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11 TEFIKLDQ 18
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Best Local Similarity
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                                                                                                                                       NCBI_TaxID=562;
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01-OCT-2003
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Matches
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Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
BIRI, C36900; C36900.
G0, G0:0003723; F:RNA binding; IEA.
InterPro; IPR002942; S4.
PROSITE, PSS0889; S4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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PROSITE; PS50889; S4: 1.
Hypothetical protein; Complete proteome.
Appother 252AC70BCBC3D094 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          68 AA; 7699 MW; 6AE9BB3FAA25753B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein CPE0003.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
ENBL. AP003185; BAB79709.1;
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002942; S4.
Pfam; PF01479; S4; 1;
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MEDLINE=21664373; PubMed=11792842;
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STRAIN=13 / Type A;
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SEQUENCE 68 AA;
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Best Local Similarity
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RESULT 14
09F572
AC 09F57
DT 01-MA
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Q8JTS8
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Q8JTS
ID Q8JTS
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Section 18.7.

A MEDLINE=96128251; PubMed=8537120;

A MEDLINE=96128251; PubMed=8537120;

A MEDLINE=96128251; PubMed=8537120;

Thentification of major histocompatibility complex genes in the "Identification of major histocompatibility complex genes in the "Identification of major histocompatibility complex genes in the "Identification of major histocompatibility complex genes in the EMBL; Z54079; CAA90785.1; "

EMBL; Z54079; CAA90785.1; "

R GO; GO:0019884; P:MHC class II receptor activity; IEA.

R GO; GO:0019884; P:mutigen processing, exogenous antigen via M. . .; I R GO; GO:0019886; P:immune response; IEA.

R GO; GO:0019886; P:immune response; IEA.

R InterPro; IPR000353; MHC II beta.

R Probon; PR0000328; MHC II beta; 1.

R Proportion; MHC III beta; 1.

R Proportion; PR000328; MHC III beta; 1.

R Proportion; PR000328; MHC III beta; 1.

R Proportion; PR000328; MHC III beta; 1.
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Afonso C.L., Tulman B.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
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Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
Kutish G.F., Rock D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Canthomorpha, Acanthomorpha, Acanthomorpha, Percomorpha, Acanthomorpha, Poeciliidae, Poecilia.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SPV090 hypothetical protein.
                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                       74 A.A.
                                                                                                                                   Created)
                                                                                       PRT;
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Mnc, class IIB protein (Fragment).
WHC, CLASS IIB.
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                                                                                                                                                                                                                                               Poecilia reticulata (Guppy)
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                                                                                         PRELIMINARY;
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24 LEFIRFDS 31
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NCBI_TaxID=10276;
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01-NOV-1996
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Q31516;
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                                         RESULT 16
Q31516
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STRAIN=Neethling Warmbaths LW;
STRAIN=Neethling Warmbaths LW;
Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
Lu Z., Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
"Molecular characterization of the South African vaccine strain and
the field isolate of lumpy skin disease virus.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AFR25528; AAK85654.1;
EMBL, AF409137; AAN02661.1;
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MEDLINE=21329495; PubMed=11435593;
MIDLINE=21329495; PubMed=11435593;
MIDMan E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Neethling 2490; Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                         100.0%; Score 25; DB 12; Length 75; 50.0%; Pred. No. 7.2e+02;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF410153; AAL68829.1; -. InterPro; IPR007952; Pox A3L. PFan, PF05288; Pox.A3L; T. Pran, PF05288; Pox.A3L; T. SEQUENCE 75 AA; B974 MW; EFF0DDB92D47E3A CRC64:
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
LSDV093 hypothetical protein.
LSDV093 OR LD093.
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4; Mismatches
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(TrEMBLrel. 24, I
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NCBL_TaxID=59509;
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

WEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Rambo T., Crane Schwartzbeck J., Thurmond S., Mao L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                       Score 25; DB 16; Length 79;
Pred. No. 7.6e+02;
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EMBL; AC037197; AAG12482.2; -..

Gramene; Q9FWI7; -..

HYDOITherical protein.

SEQUENCE 80 AA; 8891 MW; 98F6D664F8B95709 CRC64;
                                                                                                                                                                                                                         PIR, G97292, G97292.
Hypothetical protein, Complete proteome.
SEQUENCE 79 AA, 9483 MW; 20426177BEEA12F5 CRC64;
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01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Hypothetical protein.
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24 MEFINKDD 31
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Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
Lu Z., Varede F.I., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
"Molecular characterization of the South African vaccine strain and
the field isolate of lumpy skin disease virus.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF40318; AAN02818.1.
InterPro; IPRO7952; Pox A3L.
Pfam: PF05288; Pox A3L.
Hypothetical protein.
SEQUENCE 75 AA; 9022 MW; 98A41C4CAF4FECF6 CRC64;
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           Lumpy skin disease virus (LSDV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Eukaryota, Viridiplantae, Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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"REX1, a novel gene required for DNA repair.";
Biol. Chem. 0:0-0(2003).
EMBL, AV28481, AP212520.1;
SEQUENCE 78 AA, 8941 MW; 34D47D31F8161F5D CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Hypothetical protein CAC3193.
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Matches 4; Conservative
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                                                                                  NCBI_TaxID=59509;
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                                                            Capripoxvirus
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MEDLINE=22608414; PubMed=12721629;

MEDLINE=22608414; PubMed=12721629;

Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Touts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,

Rolonay J.F., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,

Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-22668415; PubMed=12721630; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Shattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N., "Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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Pred. No. 7.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 16; Length 81; 50.0%; Pred. No. 7.88+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 82 AA; 10000 MW; 1C1104962489B6AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein, Complete proteome.
SEQUENCE 81 AA, 9882 MW, 0933BB022A46379C CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus cereus (strain ATCC 14579 / DSM 31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical cytosolic protein.
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EMBL, AE017010, AAP10855.1; -.
                                                                                                                                                                                                                                                                                                                                                             Nature 423:81-86(2003).
EMBL; AE017036; AAP27869.1; -.
TIGR; BA4145; -.
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50.0%; E
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Best Local Similarity 50.03
Matches 4; Conservative
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6 MEFIKADE 13
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01-JUN-2003
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Q95HS2;
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Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBI, AL932555; CAD63935.1; -.
GQC; GO:0006790; P:sulfur metabolism; IEA.
Interpro; IPR003749; This.
                               The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 16; Length 81;
Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                   ; Score 25; DB 10; Length 80;
Pred. No. 7.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                    STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
Babl, ABO17048; AAP51792.1; -.
Hypothetical protein.
SEQUENCE 80 AA; 8891 MW; 98F6D664F8B95709 CRC64;
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AA; 8545 MW; 35FB6D6AA1897948 CRC64;
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Molybdopterin biosynthesis protein, D chain.
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MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
BA4145.
Bacillus anthracis (strain Ames).
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50.0%; E
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                                                                                             Science 300:1566-1569(2003).
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                                                                                                                                                                                                                                                                                                                                    4; Conservative
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Complete proteome.
                  STRAIN=cv. Nipponbare;
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56 QEFIADDR 63
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                  SEQUENCE FROM N.A.
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                                                                        chromosome 10
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Q81W38;
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Q88WY2; Q88WY2

RESULT 24

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Matches

RESULT 25

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Q81W38

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Ayoubi P.J., Harker A.R.,
"Whole-cell kinetics of trichloroethylene degradation by phenol
hydroxylase in a ralstonia eutropha JMP134 derivative.",
Appl. Environ. Microbiol. 64:4353-4356 (1998)
EMBL, AF065891; AAC77381.1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 2; Length 86; 50.0%; Pred. No. 8.3e+02; Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            891; AAC77381.1; -.
86 AA; 9583 MW; 6F9E4D89D5C00840 CRC64;
                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    Alcaligenes eutrophus (Ralstonia eutropha)
                                                                                                                                                                                                                                                                                                                  Putative hydroxylase component.
                                                                                                                                        PRELIMINARY;
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Best Local Similarity
**Local 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JMP134;
PubMed=9797289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=510;
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Q51940;
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Richman A.D., Herrera L.G., Nash D.;

Richman A.D., Herrera L.G., Nash D.;

"MHC Class II Beta Sequence Diversity in the Deermouse (Peromyscus amaniculatus): Implications for Models of Balancing Selection.";

"M GO: CO: C12000) to the EMBL/GenBank/DDBJ databases.

"R GO; GO: 0016021; C: integral to membrane; IEA.

"R GO; GO: 0016021; C: integral to membrane; IEA.

"R GO; GO: 0019884; P: ARTC class II receptor activity; IEA.

"GO; GO: 0019886; P: antigen processing, exogenous antigen; IEA.

"R GO; GO: 0006955; P: intumene response; IEA.

"R HO: PRO: 00555; P: intumene response; IEA.

"R HO: MRC II beta; I.

"R HO: MRC II beta; I.
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                                                                                                                                                                             Peromyscus maniculatus (Deer mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010237; AAL81439.1;
Incerpro; IRR004919; DUF662.
Ffam; PF03235; DUP262; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 85 AA; 9960 MW; B3CE50A6CFF33C4F CRC64;
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Pred. No. 8.2e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 AA; 10237 MW; 3061A008A7BE71DB CRC64;
(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PF1315.
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                                                                         01-JUN-2003 (TrEMBLrel. 24, Last annotation
MHC class II antigen beta chain (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
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26 EEFIRFDS 33
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EEFITDDP 63
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SQPM26a;
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                                                                                                                                                                                                                                                                                               Peromyscus.
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                                                                                                                                                   PEMA-EB
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2001JA6
AC Q0UIJA6
DT 01-JUJ
DT 01-JUJ
DD 01-J
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Gaps
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Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
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SPECIES=B.pickettii; STRAIN=PKO1;
MEDLINE=95172404; PubMed=7867951;
Byrne A.M., Kukor J.J., Olsen R.H.;
"Sequence analysis of the gene cluster encoding toluene-3-monoxygenase from Pseudomonas pickettii PKO1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 86;
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EMBL, AF28289; AAG40795.1; -...
GO:0004497; F:monoxygenase activity; IEA.
Hypothetical protein; Monoxygenase.
SEQUENCE 86 AA; 9604 MW; 7D50901A65635AB3 CRC64;
                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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50.0%; Pred. No. 8.3e+02;
tive 4; Mismatches 0;
                                                                                                                                                                                                                                86 AA.
                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence v
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein (Tbc2B monoxygenase).
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Best Local Similarity 50.0%
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Ouyang J., Nie Q., Zhang X.;
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NCBL TaxID=9031;
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SEQUENCE FROM N.A.

CETRAIN=306 / ATCC 13902 / XV 101;

MEDINE=20202145; PubMed=12024217;

A Ga Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A Ga Silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Nes L.M.C., do Amaral A.M., Bertolini M.C., Camargo, L.E.A.,

A Nes L.M.C., do Amaral A.M., Bertolini M.C., Camargo, L.E.A.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., El-Dorry H.,

A Carai D.E., Ferraco M.C., Greggio C.C., Gruber A.,

Rormighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Rormighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Rorali B.C., Machado M.A., Madeira A.M.B.N., Martine E.C., Machado M.J., Madeira A.M.B.N., Martine E.C., Machado M.J., Machale J., Marcin B.C., Oliveira W.C., Oliveira W.C., Oliveira W.R.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

A Perina dos Santos M., Trufffi D., Tsai S.M., White F.F.,

A Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

A Spinola L.A.F., Takita M.A., Trufffi D., Tsai S.M., White F.F.,

A Schubal J.C., Kitajima J.P.;

A Schubal J.C., Kitajima J.P.;

A Schoparison of the genomes of two Xanthomonas pathogens with differing host specificities
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STRAIN=HTBB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 16; Length 90; 50.0%; Pred. No. 8.7e+02;
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EMBL, ABOll903; AAM37408.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10209 MW; D4F880AED6935695 CRC64;
                                                                                                                                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC2631.
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4; Mismatches
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29 QEFIELDD 36
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LEFIFCDA 86
                                1 XEFIXXDX 8
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Q8ET09
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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"Inlimann H., Bschrich K.;

"Inlimann H., Bschrich K.;

"Inlimann H., Bschrich K.;

"Liver and muscle fructose-1,6-bisphosphatase isoenzyme amounts in different rabbit tissues.";

different rabbit tissues.";

different dibc.-2000) to the BMBL/GenBank/DDBJ databases.

EMBL; AJ300657; CAC19334.1;

HSSP; P00637; IBK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                ; Score 25; DB 16; Length 90;
Pred. No. 8.7e+02;
4; Mismatches 0; Indels
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Pred. No. 8.8e+02;
4; Mismatches 0; Indels
                                                                                 D2647123061E723B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA.
                       EMBL, AP004594; BAC12412.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10509 MW; D264712306
Nucleic Acids Res. 30:3927-3935(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00316; FBPase; 1. ProDom; PD001491; In_FB_phphtase; 1.
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Similarity 50.0%; 1
4; Conservative 4;
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50.0%;
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NCBI TaxID=672;
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Q8D9P7
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ge Z., Feng Y., Fox J.G.;
Helicobacter hepaticus genome: construction of an ordered cosmid library and sequence analysis of the selected genomic regions.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
BML; ARS186891; AAL16680.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015020; P:protein secretion; IEA.
FILEFPRO; IPRO01712; Bact_FHIPEP.
Feam; PF00771; FHIPEP; I.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                  100.0%; Score 25; DB 13; Length 92; 50.0%; Pred. No. 8.9e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 2; Length 95; 50.0%; Pred. No. 9.2e+02; tive 4; Mismatches 0; Indels
"Sequence of cGHR intron 9.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY327492; AAP92122.1; -.
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92 92
92 AA; 10377 MW; 5F624696942A3269 CRC64;
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95 AA; 10789 MW; BED4A41B153EBA53 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last_annotation update)
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01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Eddysone-inducible protein 71EJ.
EIG71EJ OR L71-10 OR CG7588.
                                                                                                                                                                                                                                                                                                                                                                                                     95 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flagellar biosynthesis protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                Q93EH4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seg
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SEQUENCE FROM N.A.
STRAIN=CANTON-S;
MEDLINE=96152797; PubMed=8568884;
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Best Local Similarity 50.00,
And 4; Conservative
                                                                                                                                          PRELIMINARY;
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48 VEFIELDI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=32025;
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01-JUN-2002
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NON TER
SEQUENCE
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SEQUENCE
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22466
AC 22406
AC 22406
DT 01-NO
DT 01-NO
DT 01-NO
DE Ecdys
GN E1671
CO Neopt
COC NEOP
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Wright L.G., Chen T., Thummel C.S., Guild G.M.;
"Molecular characterization of the 71E late puff in Drosophila melanogaster reveals a family of novel genes.";
J. Mol. Biol. 255.387-400 (1996).
EMBL; U23836; AAA74183.1;
EYJRBase; F8GROO14850; Eig71E).
InterPro; IPR001475; Insect_Unk.
Pfam; PF02448; L71.
SEQUENCE 95 AA; 11446 MW; 33171F38EA2826D1 CRC64;
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                                                                                                                                                                                                  100.0%; Score 25; DB 5; Length 95; 50.0%; Pred. No. 9.2e+02; Live 4; Mismatches 0; Indels
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46723F3FEBBF6189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q814L7;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein E02Al0.4.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 9.2e+02;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281053; CAD54130.1; -.
WormPep; E02A10.4; CE31898.
Hypothetical protein.
SEQUENCE 95 AA; 10397 MW; 4.
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Matches 4; Conservative
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46 LEFINSDC 53
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27 EEFIAVDC 34
                                                                                                                                                                                                                                                                                1 XEFIXXDX 8
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46 LEFINSDC 53
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
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BIG71EJ OR L71-10 OR CG7588.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 97;
                                                                                                                ; Score 25; DB 16; Length 95; pred. No. 9.2e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016805; AA010879.1; -.
                             "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016805; AA010901.1; -.
InterPro; IPR007712; Plasmid stabil.
Pfam; PF05016; Plasmid_stabil; 1.
Complete prote; Plasmid_stabil; 1.
SEQUENCE 95 AA; 10992 MW; 52D1683C38B56292 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 9.5e+02;
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4; Mismatches
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Matches 4; Conserv
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                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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08D9R7
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RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxerer B.G., Helt G., Nelson C.R., Miklog G.L.G.,
Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Boasley E.M.,
RA Ballew R.W., Borchan MR., Bouck J., Broketein P., Brottier P.,
Borkova D., Borchan MR., Bouck J., Broketein P., Brottier P.,
RA Burtis K.C., Busam D.A., Burler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Codson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz, C. Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz, C., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heinand T.J., Wei M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heinand T.J., Wei M., Harris M.,
RA Harris N.L., Mattel B., McThosh T.C., McLeof J.R., Thermal B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B., Spradling A.C., Standers B., Wan B.,
RA Shier B., Spradling A.C., Standers B., Wan B.,
RA Shier B., Spradling A.C., Standers E., Wan B.,
RA Shier B., Spradling A.C., Standers E., Wan S., Yao Q.A.,
RA Wang Z.Y., Wassarman D.A., Weinstender E., Wan S., Zhou X., Smith H.O.,
RA Wallams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Jenez A., Shier B., Shoper                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Moraxellaceae; Acinetobacter.
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red. No. 9.6e+02;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11749 MW; 0D769F1A427D2852 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA.
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InterPro; IPR003475; Insect_Unk.
Pfam; PF02448; L71; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000)
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Gaps

Q863N9

DE PACE DE PAC

RESULT 42

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MEDLINE=22423060; PubMed=12534463; Nelson R.J., Hilbert H., Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
             "Nucleotide sequence of the 3'-terminal region of carnation latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91324119; PubMed=1713905;
Meehan B.M., Mills P.R.;
"Nucleotide sequence of the 3'-terminal region of carnation latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intervirology 32:262-267(1991).
EMBL; X52627; CAA36855.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
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                                             Intervirology 32:262-267(1991).

EMBL; AJ010697; CAA09307.1; -.
GO; GO:0003676; Finucleic acid binding; IEA.
GO; GO:0006555; P:regulation of transcription, DNA-dependent; InterPro; IPR002568; Carla C4.

Ffam; PF01653; Carla C4; 1.

SEQUENCE 102 AA; I1584 MW; 4574B3FF43B46B19 CRC64;
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Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                          Length 102;
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; Score 25; DB 12; Length.
... No. le+03;
0; Indels
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SEQUENCE 102 AA; 11626 MW; 0474AFBF5FDB1B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative nucleic acid binding protein.
Carnation latent virus (CLV).
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Last annotation update)
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0TW-2003 (TrEMBLrel. 24, Created)
01-0TW-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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90 LEFIGIDL 97
                                                                                                                                                                                                                                                  1 XEFIXXDX 8
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90 LEFIGIDL 97
                                                                                                                                                                                               Local Similarity
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12164;
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                                                                                                                                                                               Query Match
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Q88LJ6
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498204; AAP19695.1: -
                                                                                                                                                                                            Gaps
                                         benzoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arctonyx collaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carnation latent virus (CLV).
Viruses; ssRNA positive-strand viruses, no DNA stage, Carlavirus.
VCBI_TaxID=12164;
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             Xu Y., Chen M., Zhang W., Lin M., "Genetic organization of genes encoding phenol hydroxylase, 1,2-dioxygenase alpha subunit and its regulatory proteins in
                                                                                                                                                           Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 101;
                                                                                                                                                  100.0%; Score 25; DB 2; Length 99
50.0%; Pred. No. 9.7e+02;
iive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ' Score 25; DB 6; Length 10
Pred. No. 9.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meenan B.m.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                            Acinecobacter calcoaceticus PHEA-2.";
Curr. Microbiol. 46:235-240(2003).
EMBL; AJ564846; CAD92311.1; -...
SEQUENCE 99 AA; 11542 MW; 11BF76425EA2D847 CRC64;
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101 AA; 11428 MW; AD696CB6E0EBD7AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                      24, Created)
24, Last sequence update)
25, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone receptor (Fragment).
MEDLINE=22617848; PubMed=12732969;
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MEDLINE=91324119; PubMed=1713905;
Meehan B.M., Mills P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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25 AEFIEFDF 32
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VEFIELDI 35
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Koepfli K.-P., Wayne R.K.;

"Type-1 STS Markers Are More Informative Than Cytochrome b in

"Type-1 STS Markers Are More Informative Than Cytochrome b in

Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Mus muscallus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 6; Length 105; Pred. No. 1e+03;
                                                                                                                                                                                        Length 105;
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                                                                                                                                                                                                                                0; Indels
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105 105
105 AA; 11852 MW; F07A7052451EB8E7 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                            DB 6;
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EMBL, AF498199; AAP19690.1; -...GO, GO:0004872; F:receptor activity; IEA.
                         Syst. Biol. 0:0-0(2003).
EMBL; AF498187; AAP19678.1;
GO; GO:0004872; F:receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created. 01-JUN-2003 (TrEMBLrel. 24, Last 8et 01-OCT-2003 (TrEMBLrel. 25, Last and Growth hormone receptor (Fragment).
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50.0%;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 VEFIELDI 39
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105 1
105 AA;
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32 VEFIELDI 39
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Best Local Similarity
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Ohdan K., Kuriki T., Takata H., Okada S.;
Cloning of the cyclodextrin glucanotransferase gene from alkalophilic actions of the raw starch-binding domain.";
Appl. Microbiol. Biotechnol. 53:430-434(2000).
BMBL; AB01570; BAA31532.1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae;
                   Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
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KOOPÍLI K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 16; Length 102;
Pred. No. 1e+03;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 2; Length 105; 50.0%; Pred. No. 1e+03;
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12243 MW; 9677A516E4C4916B CRC64;
                                                                                                                                                                                                                                                                                                              9A2E2D606938A8A5 CRC64;
                                                                                                                          "Complete genome sequence and comparative analysis of metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
EMBL; ADMOSTARIA ADMOSTARIA - TIGR; PP1935; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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4; Mismatches
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live 4; Mismatches
                                                                                                                                                                                            GO, GO.0003677; F.DNA binding; IEA.
InterPro: IPR001387; HTH_3.
Pfan; PF01381; HTH_3; 1.
Complete proteome.
SEQUENCE 102 AA.
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01-NOV-1998 (TrEMBLrel. 08, Le
01-DEC-2001 (TrEMBLrel. 19, La
A2-5a orf4.
Bacillus sp.
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Best Local Similarity 50.v.
74 Conservative
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82 NEFIGFDI 89
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78 AEFINGDP 85
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Best Local Similarity
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AC Q863Q
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106 AA; 12003 MW; EFB0DDAEA24C29FF CRC64;
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50.0%; Pred. No. 1e+03;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                      107 AA
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                                                                                                 Query Match
Best Local Similarity 50.00,
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34 VEFIELDI 41
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Best Local Similarity
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"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalla: Carnivora)."; Syst. Biol. 0:0-0(203).
EMBL; AF498190; AAP19681.1; -.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";
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Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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                                                                                                                            Score 25; DB 11; Length 105;
Pred. No. 1e+03;
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                                                                                    12193 MW; BICBD28D2FB01797 CRC64;
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106 106
106 AA; 12006 MW; BFB0CGDB793AE9FF CRC64;
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01-UDM-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL: AF498191; AAP19682.1; -...
GO; GO:0004872; F:receptor activity; IEA.
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60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO848669; BAC39298.1; -.
Hypochhetical protein.
SEQUENCE 105 AA; 12193 MW;
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79 LEFINEDY 86
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Nobell X.-B., Warkers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF499184; AAP19675.1;
GO; GO:0004872; F:receptor activity; IBA.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).

EMBL, AF499185; AAP19676.1;

GO: 0004872; F:receptor activity, IEA.
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                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                1 107 107 107 12101 MW; 7F3D579D3C26011B CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Local Similarity 50.0 ses 4; Conservative
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34 VEFIELDI 41
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34 VEFIELDI 41
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Best Local Similarity
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NON TER
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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                                                                                                                   100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; tive 4; Mismatches 0; Indels
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              1 1
107 107
107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;
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Last annotation update)
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01-JTM-2003 (TrEMBLrel. 24, Last sequence update)
01-JTM-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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Pred. No. 1e+03;
4; Mismatches
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EMBL; AF499188; AAP19679.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Syst. Biol. 0:0-0(2003).
EMBL; AF498186; AAP19677.1; -.
GO; GO:0004872; F:receptor activity; IEA
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50.0%; Pre-
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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34 VEFIELDI 41
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34 VEFIELDI 41
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
EMBL; AR498192; AAP19683.1;
"EMBL; AR498192; AAP19683.1;
"Exceptor activity; IEA.

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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498189; AAP19680.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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4; Mismatches 0; Indels
                                                                       Length 107;
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107 107
107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JTN-2003 (TrEMBLrel. 24, Created)
01-JTN-2003 (TrEMBLrel. 24, Last sequence update)
01-JTN-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                          DB 6;
                                                                                                        50.0%; Pred. No. 1e+03;
tive 4; Mismatches
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                                                                                100.0%; Score 25;
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34 VEFIELDI 41
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34 VEFIELDI 41
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Q863P8;
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).
EMBL; AF498193; AAP19684.1;
GO; GO:0004872; F:receptor activity, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
                                             Gaps
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Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustellinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mustela frenata (Long-tailed weasel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
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                      ; Score 25; DB 6; Length 107;
Pred. No. 1e+03;
4; Mismatches 0; Indels
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 12137 MW; 96DBCA309E7789FE CRC64;
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107 107
107 AA; 12140 MW; 96DBD146450149FE CRC64;
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107 AA; 12140 MW; 96DBD146450149FE CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                   107 AA
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EMBL; AF498194; AAP19685.1; -.
GO; GO:0004872; F:receptor activity; IEA
                                                                                                                                                      Created)
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                                         4; Conservative
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0 Matches 4; Conservative
                                                                                                                                                                                                    Mustela erminea (Ermine)
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34 VEFIELDI 41
                                                          1 XEFIXXDX 8
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VEFIELDI 41
 107 AA;
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                 Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=36723;
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                                     Matches
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"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).

EMBL; AF498195; AAP19686.1; -.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).
EMBL; AR498196; AAP19687.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Mustela vison (American mink).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Rissipedia; Mustelidae; Mustelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martes americana (American marten).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 6; Length 107;
                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA; 12149 MW; 96CCE146450149FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA; 12172 MW; 96DBD14658B649FE CRC64;
                                                                                                                                                                                                                                                                                                    01-0UN-2003 (TrEMBLrel. 24, Created)
01-0UN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT--2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24, Last sequence update)
25, Last annotation update)
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                                                                                                                                                                                                                                                                    107 AA
                             Pred. No. 1e+0
4; Mismatches
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Koepfli K.-P., Wayne R.K.; "Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelldae (Mammalia: Carnivora).";
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KROEPELI K.-P., Wayne R.K.;

Type-1 STS Markers Are More Informative Than Cytochrome b in

Type-1 STS Markers Are More informative Than Cytochrome b in

Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";

Syst. Biol. 00-0(2003).

Syst. Biol. 00-0(2003).

Syst. Biol. 00-0(2003).

GO, GO:0004872; Freceptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ictonyx striatus (striped polecat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12140 MW; 96DBD146450149FE CRC64;
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107 107
107 AA; 12109 MW; 4048E64F61DBF52C CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                                                                                                                                                Growth hormone receptor (Fragment). 24, Created) 01-0TM-2003 (TrEMBLrel. 24, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Growth hormone receptor (Fragment).
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 Pred. No. 1e+(
1; Mismatches
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EMBL; AF498201; AAP19692.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                      PRT;
   50.0%;
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                   4; Conservative
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34 VEFIELDI 41
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107 AA;
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34 VEFIELDI 41
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Best Local Similarity
                                                    1 XEFIXXDX 8
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Matches 4; Conserv
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   Best Local Similarity
Matches 4; Conserv
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Q863P2
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AR498198; AAP19689.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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Similarity 50.0%; Bred. No. 1e+03;
4; Conservative 4; Mismatches 0; Indels
            Score 25; DB 6; Length 107;
                                             0; Indels
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Last annotation update)
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                             Pred. No. 1e+03;
4; Mismatches
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EMBL; AF498197; AAP19688.1; -.
GO; GO:0004872; F:receptor activity; IEA
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Growth hormone receptor (Fragment)
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Query Match
Best Local Similarity 50...
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34 VEFIELDI 41
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34 VEFIELDI 41
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01-JUN-2003
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SEQUENCE FROM N.A.

Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Bassariscus.
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Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Melinae,
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107 107
107 AA; 12141 MW; C671DBEC450C29F3 CRC64;
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                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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01-07D-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                   107 AA
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EMBL; AF498206; AAP19697.1;
                                                                                                                 PRELIMINARY;
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34 VEFIELDI 41
            1 XEFIXXDX 8
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VEFIELDI 41
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                                                                                                                                                                                                                   Melogale moschata.
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Matches 4; Conserv
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"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL: AF498202; AAP19693.1; -...
GO: GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                               Meles meles (Eurasian badger).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae; Meles.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
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Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Taxidiinae;
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      Indels
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Last sequence update)
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                                                                                                                                    107 AA.
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    4; Mismatches
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EMBL; AF498203; AAP19694.1; -.
GO; GO:0004872; F:receptor activity; IEA
                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created 01-JUN-2003 (TrEMBLrel. 24, Last sec 01-OCT-2003 (TrEMBLrel. 25, Last and Growth hormone receptor (Fragment).
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34 VEFIELDI 41
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VEFIELDI 41
                           1 XEFIXXDX 8
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            RESULT 72
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STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=2228563; PubMed=12397186;
Addic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                  Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Mammalia, Eutheria, Carnivora, Fissipedia, Procyonidae, Procyon.
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EMBL, AE014982; AAN59158-1; -

Hypothetical protein; Complete proteome.

SEQUENCE 107 AA; 12770 MW; CEIA07D27B28AEC0 CRC64;
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107
107 AA; 12024 MW; 96CB24F6501459BB CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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                                                                                                     107 AA
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EMBL; AF498207; AAP19698.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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                                                                                                                                                                                                                                                    (Raccoon)
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DEFIGYDR 27
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34 VEFIELDI 41
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
34 VEFIELDI
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SEQUENCE
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Q8DT70
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MEDLINE-2709201; PubMed=12810954;
MEDLINE-2709201; PubMed=12810954;
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                            Salamoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Willey M., Genome Sequence of the plant pathogen Ralstonia solanacearum.";
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                                                                                                                                                            Raistonia solamacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Raistonia.
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SEQUENCE 108 AA; 12836 MW; 93DABA05000CDB51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA; 12298 MW; 2D5E38CE1C7E24EC CRC64;
                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable phage HK022 GP9-related protein.
RSC1686 OR RSO4080.
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Last annotation update)
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50.0%; Pred. No. 1.1e+03;
cive 4; Mismatches 0;
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108
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Interpro; IPR006453; Gp16_SPP1.
TIGRFAMS; TIGR01563; Gp16_SPP1; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                           STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
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     PRELIMINARY;
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45 KEFIAADR 52
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SEQUENCE 108 AA;
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                                                                     59 IEFIDKDL 66
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84 IEFICLDL 91
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"Full leng
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Q41901;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                 Zehr J.P., Jenkins B.D., Short S.M., Steward G.F.;
"Nitrogenase gene diversity and microbial community structure: a cross-system comparison.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY223946; AA067605.1;
EMBL; AY223946; AA067611;
GO; GO:0005524; F.AFP binding; IEA.
GO; GO:0005524; F.AFP binding; IEA.
GO; GO:000518; P:oxidoreductase activity; IEA.
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Currie J., Collura K.;
"Rice Genomic Sequence.";
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50.0%; Pred. No. 1.16+03;
iive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11768 MW; 2A3FADB64DBF4269 CRC64;
                                                                                                                                                              01-JUN-2003 (TrEWBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Dinitrogenase reductase Fe protein (Fragment).
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Last annotation update)
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                                                                                                                                     109 AA.
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Pfam; PF00142; fer4 Nifh; 1
PRINTS; PR00091; NITROGMASEII.
PROSITE; PS00746; NIFH_FRXC 1; 1
PROSITE; PS00692; NIFH_FRXC 2; 1.
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23,
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                                                                                                                                                                                                                                                               Gamma-proteobacterium Hot
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1 XEFIXXDX 8
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE
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Q83UP9
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Q8H8H2
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NADH ubiquinone oxidoreductase subunit.
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Maiglantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maignoliophyta; euclioctyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Columbia; TISSUE=Green siliques;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z17587; CAA79002.1; -.
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Feldmann K.A., Flavell R.B., White O., Salzberg S.L.,
"Full-length messenger RNA sequences greatly improve genome
annotation.";
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Pred. No. 1.1e+03;
4; Mismatches 0; Indels (
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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   110 AA
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01-OCT-2000 (TrEMBLrel. 15, Last seq
PRT;
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Bolotin A., Wincker P., Mager S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sp. lactis ILIA03.";
Genome Res. 11.731-753 (2001).
EMBL; ABO06372; AAK05505.1;
ETR; G86800; G86800.
Complete proteome.
SEQUENCE 114 AA; 12458 MW; C5AD66755D6DFF0C CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=21113149; PubMed=11160885; Chopin A., Chopin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin A., Hallysis of eix prophages in Lactococcus lactis IL1403: different genetic structure of temperate and virulent phage populations."; Nucleic Acids Res. 29:644-651(2001).
                                                                                                                                                                                                                                                                               no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF323669; AAK08317.1; - 137B66755565F7AE CRC64;
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; Score 25; DB 9; Lengu...
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4; Mismatches
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MEDLINE=21235186; PubMed=11337471;
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PI334 OR LL1407.
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Viruses; dsDNA viruses,
NCBL_TaxID=151536;
                                                               PRELIMINARY;
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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22 GEFIVCDE 29
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SEQUENCE FROM N.A.

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MEDLINE=22247741; PubMed=12271122;

MEDLINE=22247741; PubMed=12271122;

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Madupu R.,

Anglerty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Read T.D., Lindler L.B., Halling S.M., Bayles S.L.,

Riedmuller S., Tettelin H., Gill S.R., White O., Salbberg S.L.,

Anover D.L., Lindler L.B., Halling S.M., Boyle S.M., Fraser C.M.;

The Brucella suis genome reveals fundamental similarities between

The Brucella and plant pathogens and symbionts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

REMBL, ARO1433; AAN29155.1; -.

REMBL, ARO1433; Complete proteome.

PR Fram, PPOSSIO; DUF779.

PR Fram, PPOSSIO; DUF779.

PR Hypotherical protein; Complete proteome.

SQ SEQUENCE 110 AA, 11720 MW; 0862D9576C1GEEF33 CRC64;
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Pred. No. 1.1e+03;
4; Mismatches 0; Indels
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Brucellaceae, Brucella.
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               Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.; "Full-Length cDNA from Arabidopsis thaliana."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 110 AA; 12234 MW; 8E81416C52B9C437 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
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EMBL, AR325039, AAG40391.1;

EMBL, AX087471, AAM55015.1;

EMBL, BT004574, AAQ42820.1;
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SEQUENCE FROM N.A
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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
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                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Bin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones.";
DNA Res. 7:131-135(2000).
EMBL; AB024036; BAB02814.1; -.
POTTENCE 115 AA; 13512 MW; 81A9D45FFF0B9DC4 CRC64;
                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                 115 AA.
             PRT;
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MEDLINE=21156231; PubMed=11258796;
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Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

EMBL, AB017164, AA000101.1; -. Complete proteome
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MEDLINE=22508414:
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                  Length 116;
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                                       PIR, A85636, A85636.

PIR, E90773, E90773.

Hypothetical protein; Complete protecme.

SEQUENCE 116 AA; 13270 MW; 48017DE2635A5A6F CRC64;
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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50.0%; Pred. No. 1.1e+03;
11ve 4; Mismatches 0;
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EMBL; AE005294; AAG55549.1; ~.
EMBL; AP002554; BAB34580.1; ALT_INIT.
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STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486;
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11 PEFIFNDN 18
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4 PEFIATON 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prochlorococcus.
NCBI_TaxID=1219;
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RA RA RA RA RA RT RT DR DR SQ

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SEQUENCE FROM N.A.

STRAIN-EI TOR NIGSGI / Serctype 01;

MEDLINE-20406833; PubMed=10952301;

Meidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

GILL S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragori I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDILINE=22336326; PubMed=12446651;

Cheng Y.Q., Tang G.L., Shen B.;

"Identification and Localization of the Gene Cluster Encoding
Identification and Localization of the Anticumor Macrolactam Leinamycin in Streptomyces
Biosynthesis of the Antitumor Macrolactam Leinamycin in Streptomyces
atroclivaceus S-140.";

J. Bacteriol. 184:7013-7024(2002).

EMBL. AFG4855; ARMS535.1; -.

Hypothetical protein.

SEQUENCE 120 AA, 14105 MW; 95BC6B553E2940D1 CRC64;
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                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Pred. No. 1.2e+03;
4; Mismatches 0; Indels 0
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 1.28+03;
4; Mismatches 0; Indels
        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                       Interproj TR007712; Plasmid stabil.
Pfam; PF05016; Plasmid stabil; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 119 AA; 13609 MW; 8CC94AB091E3C8C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.MAR-2003 (TrEMBLrel. 23, Created)
01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
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50.0%; F
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50.0%; E
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Best Local Similarity 50...
Loca 4; Conservative
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                                                                                                                                                                                                                                                                                                               cholerae.";
Nature 406:477-483(2000)
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Best Local Similarity
Matches 4; Conserv
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Vibrio cholerae.
                                                      NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                   "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 16; Length 118; 50.0%; Pred. No. 1.2e+03;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE016998; AAP07302.1; -.
InterPro; IPR006542; Cons_hypoth1655.
ITIGREAMS; ITGR01655; yraw.fam, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 118 AA; 13830 MW; C307191648AFB9FA CRC64;
                                                                                                                                                                                                                                         InterPro; IPR006542; Cons_hypoth1655.
TIGREAMs; TIGR01655; yxeA_fam; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 118 AA; 13876 MW; BAE8EA7328AE91CE CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VCA0423.
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Last annotation update)
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4; Mismatches
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EMBL; AE017024; AAP24263.1; -.
TIGR; BA0219; -.
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Best Local Similarity 50.03
Matches 4; Conservative
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Nature 423:87-91(2003)
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Best Local Similarity
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                                                                                                                             Fraser C.M.;
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Q81IW3; Q811W3

RESULT 85

à a Q811W3

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RESULT 86

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Q9KMD8

SE PT PT SE

Matches

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STRAIN-16M, ATCC 23456 / Biotype 1;
MEDLINE-20020109; PubMed=11756688;
MEDLINE-20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharvya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov B., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen Prucella melitensis."
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=MR-1;
MEDLINE=22297686; PubMed=12368813;
MEDLINE=22297686; PubMed=12368813;
Medderg J.F., Paulson I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Rad T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umrayam L.A., White D.H., Kolonay J.F., Madupu R., Peterson J.D., Umrayam L.A., White O., Wolf A.M., Vanathevan J., Weldan J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
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                                                                                                                                                                                                                                         Brucella melitensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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Hypothetical protein; Complete proteome.
SEQUENCE 123 AA; 13129 MW; 2ECEC95F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraheme cytochrome c, putative.
                                                                                                                                                                                                           Hypothetical protein BMEI1745
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NCBI_TaxID=70863;
                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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InterPro; IPR008497; DUF779.
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      89 REFIHDDK 96
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57 GEFIVGDT
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SEQUENCE 1
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Q8EH18;
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Matches
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                                                                                                                                                                                                                                         Sasaki Y., Ishikawa U., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshimo C., Horino A., Shiba T., Sasaki T., Hattori M.;
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res 30:5293-5300(2002).
BMBL, Ab004170; BAC43825.1;
GO; GO:0016740; Firtansferase activity; IEA.
GO; GO:0016740; Firtansferase activity; IEA.
InterPro; IPR008278; 4-PPT_transf.
InterPro; IPR008282; ACPS.
InterPro; IPR004588; Pantethn_trn.
PFIGM: PFIO4684 PAPPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 824 / DSM 792 / VKM B-1787,
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.M., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                        Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                   01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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TIGRFAMS; TIGR00556; pantethn_trn; 1.
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                                                        Holo-acyl carrier protein synthase.
                                                                                                                                                                                                                          MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE007821; AAK81191.1; -
PIR; D97300; D97300.
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4; Conservative
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Predicted membrane protein.
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                                                                                                     Mycoplasma penetrans.
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83 IEFIKNDN 90
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SEQUENCE 120 AA;
                                                                                                                                                                                 SEQUENCE FROM N.A.
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Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R. Rambo T., Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
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MEDLINE=21145866; PubMed=11248100;
MEDLINE=21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
May B.J., Zhang Q., Li L.L., Paustian multocida Pm70.";
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006157; AAK03255.1;
InterPro: IPR00520; Cons. hypoth156.
Pfam; PF04076; DUF388; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 124 AA; 13402 MW; 289E9736A09BBAA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-C. sativa (japonica cultivar-group); STRAIN-cv. Nipponbare; Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116600; AAN04141.1; -.
EMBL; AC098696; AAN04101.1; -.
EMBL; AE017059; AAP52225.1; -.
                                                                                                                                                                                                                                                                                                                   SPECIES=0.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare; The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gramene, Q8L3Q2; -.
Hypothetical protein.
SEQUENCE 124 AA; 12871 MW; FB3B4ED959E4C1E8 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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DEFIFRDV 76
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67 AEFISPDH 74
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Hypothetical protein.

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MEDLINE=21472264; PubMed=11587856;
MEDLINE=21472264; PubMed=11587856;
Moreland A.L., Whitmire W.M., Kamper S.M., Simbi B.H., Ganta R.R., Moreland A.L., Mwangi D.M., McGuire T.C., Mahan S.M.;
"A subset of Cowdria runinantium genes important for immune recognition and protection.";

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Anaplasmataceae; Ehrlichia.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2003 (TrEMBLrel. 24, Last annotation update)
11-UNN-2003 (TrEMBLrel. 24) Last annotation update)
14yporthetical dimethyl adenosine transferase (Fragment).
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                      GO; GO:0005489; F:electron transporter GO; GO:0006118; P:electron transport; I InterPro; IRR000345; CytC heme BS. PROSITE; PSC0190; CYTOCHRÖME_C; 4. Complete proteome.

SEQUENCE 123 AA; 13307 MM; S60FE1AC
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Camacho A., Vinuela E.; "protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells."; Virology 181:251-257(1991).
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Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.;
"African swine fever virus encodes two genes which share significant
homology with the two largest subunits of DNA-dependent RNA
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MEDLINE=93346971; PubMed=8393914;
Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E
"African swine fever virus thymidylate kinase gene: sequence and
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MEDLINE=90357780; PubMed=2389555;
Blasco R., Lopez-Otin C., Munoz M., Bockamp E.O., Simon-Mateo C.,
                                                                                                                                                                                                                                                                                                                                           families in African swine fever virus: family 505.";
                                                                                                                                                                                                                                                                         MEDLINE=94187118; PubMed=8139051;
Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
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Yanez R.J., Rodriguez J.M., Boursnell M., Rodriguez J.F.,
"Two putative African swine fever virus helicases similar
                                                                                                                                                                  Almazan F., Murguia J.R., Rodriguez J.M., La Vega I., V. Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
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Nucleic Acids Res. 21:2423-2427(1993).
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J. Virol. 68:2746-2751(1994).
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MBDLiARE=96036500; PubMed=7483270;
Yanez R.J., Rodriguez J.R., Nogal M.L., Yuste L., Enriquez C.,
Rodriguez J.F., Vinuela E.,
"Immune protection conferred by the baculovirus-related glycoprotein
Of Thogoto virus (Orthomyxoviridae).";
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"The complete sequence of Pseudomonas putida bacteriophage gh-1: A member of I7 family of viruses.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493143; AAO73158.1;
                                                                     RNA stage; Caudovirales; Podoviridae;
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La Vega I., Blasco R., Vinuela E.,
"Multigene families in African swine fever virus: family 360.";
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"Multigene families in African swine fever virus: family 110.";
J. Virol. 64:2064-2072(1990).
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Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
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SEQUENCE 127 AA; 14190 MW; F38DB58355D3A48D CRC64;
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MEDLINE=94233765; PubMed=8178480;
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MEDLINE=90219205; PubMed=2325203;
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MEDLINE=90219204; PubMed=2325202;
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MEDLINE=91134988; PubMed=1994575;
01-JUN-2003 (TrEMBLrel. 24,
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                                          Pšeudomonas phage gh-1.
Viruses; dsDNA viruses, no
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Vinuela E.;

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"A gene homologous to topoisomerase II in African swine fever virus.";
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                                                                                                       Lopez-Otin C., Freije J.M., Parra F., Mendez E., Vinuela E., "Mapping and sequence of the gene coding for protein p72, the major capsid protein of African swine fever virus."; Virology 175:477-484 (1990).
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pre-mRNA processing proteins and vaccinia virus ATPases D11L
                                                                                                                                                                                                                                                                                                                                    MEDLINE=93327788; PubMed=8335009;
Simon-Mateo C., Andres G., Vinuela E.;
"Polyprotein processing in African swine fever virus: a novel gene
expression strategy for a DNA virus.";
EMBO J. 12:2977-2987(1993).
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MEDLINE=99174941; PubMed=8382399;
MEDLINE=99174941; PubMed=8382399;
Pena L., Yanaz R.J., Revilla Y., Vinuela E., Salas M.L.;
"African swine_fever virus guanylyltransferase.";
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STRAIN=BA71V;
MEDLINE=93233210; PubMed=8474154;
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Yanez R.J., Vinuela E.;
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                                  Gene 134:161-174(1993)
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Lee H.J., Essani K., Smith G.L.;
"The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
Virology 281:170-192(2001).
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                                          STRAIN=BA71V;
MEDLINE=94091056; PubMed=8266720;
MEDLINE=94091056; PubMed=8266720;
Freije J.M., Lain S., Vinuela E., Lopez-Otin C.;
"Nucleotide sequence of a nucleoside triphosphate phosphohydrolase gene from African swine fever virus.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Nesomyinae;
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Thesis (2000), Sir William Dunn School of Pathology, University
EMBI: A.7293568; CAC21279.1; -.
SEQUENCE 129 AA; 15281 MW; 34340C6771199E90 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class II antigen (Fragment).
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98 IEFIITDT 105
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NCBI_TaxID=89379;
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RA Sommer S., Tichy H.;

Ray major histocompatibility complex (MHC) class II polymorphism and paternity in the monogramous Hypogeomys antimena, the endangered,

RT paternity in the monogramous Hypogeomys antimena, the endangered,

RT paternity in the monogramous Hypogeomys antimena, the endangered,

RT paternity in the monogramous Hypogeomys antimena, the endangered,

RT paternity in the monogramous Hypogeomys antimena, the endangered,

RT paternity in the monogramous Hypogeomys antimena, the moline REBL, A01334867. Class II receptor activity; IEA.

GG; GG:0016021; F:MHC class II receptor activity; IEA.

GG; GG:0019886; P:antigen presentation, exogenous antigen; IEA.

GG; GG:0019886; P:antigen presentation, exogenous antigen via M. . .; IEA.

GG; GG:0019886; P:antigen presentation, exogenous antigen via M. . .; IEA.

GG; GG:0019886; P:antigen presentation, exogenous antigen via M. . .; IEA.

GG; GG:0019886; P:antigen presentation, exogenous antigen via M. . .; IEA.

InterPro; IPRO0103; MHC_II_alpha.

RT InterPro; IPRO0103; MHC_II_alpha.

RT RT PRO9193; MHC_II_alpha; 1.

SMART; SMO0407; IGG1; 1.

RNART; RNART; RNORTED: MHC_II_Transmembrane.
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Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; endicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Plsum.
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"Expression of the NADP-thioredoxin reductase/thioredoxins h system during germination of seeds of Pisum sativum L.";
Submitted (OCT-2002) to the BME/GenBank/DDBJ databases.
EMBL; AY17051; AA012855.1; --
GO; GO:0006489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR006662; Thiored.
InterPro; IPR005746; Thiored.
InterPro; IPR005745; Thiored.
InterPro; IPR00663; Thiored.
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50.0%; Pred. No. 1.38+03;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=99376745; PubMed=10447867;
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PRINTS; PR00421; THIOREDOXIN.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Growth hormone receptor (Fragment).
Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Fathimani K., Hull K., Harvey S.;
Sequence analysis of the intracellular domain of rodent growth hormone receptor CDNAS.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241184; AAK28386.1;
GO; GO:0004872; F:receptor activity; IEA.
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